

09/830807

GJE-65

## SEQUENCE LISTING

JG08 Rec'd PCT/PTO 30 APR 2001

<110> Crooke, Helen R.  
Clarke, Enda E.  
Everest, Paul H.  
Dougan, Gordon  
Holden, David W.  
Shea, Jacqueline E.  
Feldman, Robert G.

<120> VIRULENCE GENES AND PROTEINS, AND THEIR USE

<130> GJE-65

<140>

<141>

<160> 72

<170> PatentIn Ver. 2.1

<210> 1

<211> 4333

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1017)..(2549)

---

<400> 1

ccattactca gaatgggcgg atacacaata aaaattgttc ttcttattac cgcataaccg 60  
atgccgaggc acaaaaaaat caccgatagt ttaccatcg agaatttttt attcgtttta 120  
tcagaatttt ctaaattatt tctgatacgt ttgaatatcc agacgcacag cgtcgtcatg 180  
accactaaca ccagtaaaaa ccacaggtgt gatattaatt cccaggccaa cgtattatat 240  
ttgtcataca atgacagtcc aggccaactt tccgctttcc ctttgacgta ttgcagcata 300  
ataaattgcg gcaatgtcag taggggggatg gctgttaaca tcgggatacc tacacgttcg 360  
acacgtactt tccaccattt tttcaaggga tagcgtaaaa aaagcatgta ggaaaagtac 420  
ccggatataa cgaaaaatac ctgcatgcgg aacgagtggg tgaagtcatt aaaaagggtc 480  
agccataatg acggttcggc gctattcaca tgccatgtat ggctcgaata gattaaagaa 540  
atatgaaaag ggatccctaa caacatcagc caggcgcgga tggagtcgag gaaatattca 600  
cgttgcgcgg gtactgggtt catatatggt taactaatct cggatttttc gtcttatccc 660  
tgtcgggtta tgcctttagg cttgttgcca tagcgacacc gacctgaccg cgccaggcgc 720  
aggcttcaag gtttttatgc atagcatcat cgctaccact aaccagaatg gaagcgtctg 780

taagacgggtt gataaataaa tttgctggca aaccctacac gaagtcgatg cttctgtctt 840  
 taggagaagc acggaaagtg aaaacggttg caatcaggtg cttaatccat gagccagtgt 900  
 gctgaacgat accgggattc tgttgtcgga atggcaggtt atccattaaa atagatcgga 960  
 tcgatataag cacacaaagg gggaagtgt tactaattat gaaacataaa ctacaa atg 1019  
 Met  
 1  
 atg aaa atg cgt tgg ttg agt gct gca gta atg tta acc ctg tat aca 1067  
 Met Lys Met Arg Trp Leu Ser Ala Ala Val Met Leu Thr Leu Tyr Thr  
 5 10 15  
 tct tca agc tgg gct ttc agt att gat gat gtc gca aag caa gct caa 1115  
 Ser Ser Ser Trp Ala Phe Ser Ile Asp Asp Val Ala Lys Gln Ala Gln  
 20 25 30  
 tcc tta gcc ggg aaa ggc tat gag gcg ccc aaa agc aac ttg ccc tcc 1163  
 Ser Leu Ala Gly Lys Gly Tyr Glu Ala Pro Lys Ser Asn Leu Pro Ser  
 35 40 45  
 gtt ttc cgc gat atg aaa tac gcg gac tat cag cag atc cag ttt aat 1211  
 Val Phe Arg Asp Met Lys Tyr Ala Asp Tyr Gln Gln Ile Gln Phe Asn  
 50 55 60 65  
 cat gac aaa gcg tac tgg aac aat ctg aag acc cca ttc aaa ctc gag 1259  
~~His Asp Lys Ala Tyr Trp Asn Asn Leu Lys Thr Pro Phe Lys Leu Glu~~  
 70 75 80  
 ttc tac cat cag ggt atg tac ttc gat acc ccg gtc aaa ata aat gaa 1307  
 Phe Tyr His Gln Gly Met Tyr Phe Asp Thr Pro Val Lys Ile Asn Glu  
 85 90 95  
 gtg act gcc acc gca gtc aaa cga atc aaa tac agc ccg gat tat ttc 1355  
 Val Thr Ala Thr Ala Val Lys Arg Ile Lys Tyr Ser Pro Asp Tyr Phe  
 100 105 110  
 act ttc ggc gat gtt cag cat gac aaa gac acg gta aaa gac ctt ggt 1403  
 Thr Phe Gly Asp Val Gln His Asp Lys Asp Thr Val Lys Asp Leu Gly  
 115 120 125  
 ttt gcc ggt ttc aaa gtg ctt tac ccg atc aac agc aaa gat aaa aac 1451  
 Phe Ala Gly Phe Lys Val Leu Tyr Pro Ile Asn Ser Lys Asp Lys Asn  
 130 135 140 145  
 gat gaa atc gtc agc atg ctc ggg gcc agc tat ttc cgc gtg att ggt 1499  
 Asp Glu Ile Val Ser Met Leu Gly Ala Ser Tyr Phe Arg Val Ile Gly  
 150 155 160  
 gca ggt cag gtt tat ggc ctt tct gca cgc ggc ctg gca att gat acc 1547

Ala Gly Gln Val Tyr Gly Leu Ser Ala Arg Gly Leu Ala Ile Asp Thr	
165 170 175	
gcc ttg cca tcg ggt gaa gaa ttt cca cgc ttc aaa gag ttc tgg atc	1595
Ala Leu Pro Ser Gly Glu Glu Phe Pro Arg Phe Lys Glu Phe Trp Ile	
180 185 190	
gag cgt cca aaa ccg act gat aaa cgt tta acc att tat gca ttg ctt	1643
Glu Arg Pro Lys Pro Thr Asp Lys Arg Leu Thr Ile Tyr Ala Leu Leu	
195 200 205	
gac tcg ccg cgc gcg aca ggt gct tac aaa ttc gta gtt atg cca gga	1691
Asp Ser Pro Arg Ala Thr Gly Ala Tyr Lys Phe Val Val Met Pro Gly	
210 215 220 225	
cgt gac acg gtt gtg gat gtg cag tcg aaa atc tat ctg cgc gat aaa	1739
Arg Asp Thr Val Val Asp Val Gln Ser Lys Ile Tyr Leu Arg Asp Lys	
230 235 240	
gtc ggc aaa ctg ggg gtt gca ccg tta acc agt atg ttc ctg ttt ggg	1787
Val Gly Lys Leu Gly Val Ala Pro Leu Thr Ser Met Phe Leu Phe Gly	
245 250 255	
ccg aac caa ccg tcg cct gca aat aac tat cgt ccg gag ttg cac gac	1835
Pro Asn Gln Pro Ser Pro Ala Asn Asn Tyr Arg Pro Glu Leu His Asp	
260 265 270	
tct aac ggt ctg tct atc cat gct ggt aat ggc gaa tgg atc tgg cgt	1883
Ser Asn Gly Leu Ser Ile His Ala Gly Asn Gly Glu Trp Ile Trp Arg	
275 280 285	
ccg ttg aat aac ccg aaa cat tta gcg gtc agc agc ttc tcg atg gaa	1931
Pro Leu Asn Asn Pro Lys His Leu Ala Val Ser Ser Phe Ser Met Glu	
290 295 300 305	
aac ccg caa ggc ttc ggt cta ttg cag cgt ggt cgt gat ttc tcc cgc	1979
Asn Pro Gln Gly Phe Gly Leu Leu Gln Arg Gly Arg Asp Phe Ser Arg	
310 315 320	
ttt gaa gat ctc gat gat cgt tac gat ctt cgt cca agc gca tgg gtg	2027
Phe Glu Asp Leu Asp Asp Arg Tyr Asp Leu Arg Pro Ser Ala Trp Val	
325 330 335	
act ccg aaa ggg gag tgg ggc aaa ggc agc gtt gag ctg gtg gaa att	2075
Thr Pro Lys Gly Glu Trp Gly Lys Gly Ser Val Glu Leu Val Glu Ile	
340 345 350	
cca acc aac gat gaa acc aac gat aac atc gtc gct tac tgg acg ccg	2123
Pro Thr Asn Asp Glu Thr Asn Asp Asn Ile Val Ala Tyr Trp Thr Pro	
355 360 365	

```

gat cag ctg ccg gag ccg ggt aaa gag atg aac ttt aaa tac acc atc 2171
Asp Gln Leu Pro Glu Pro Gly Lys Glu Met Asn Phe Lys Tyr Thr Ile
370 375 380 385

acc ttc agc cgt gat gaa gac aaa ctg cat gcg cca gat aac gca tgg 2219
Thr Phe Ser Arg Asp Glu Asp Lys Leu His Ala Pro Asp Asn Ala Trp
390 395 400

gtg caa caa acg cgt cgt tca acg ggg gat gtg aag cag tcg aac ctg 2267
Val Gln Gln Thr Arg Arg Ser Thr Gly Asp Val Lys Gln Ser Asn Leu
405 410 415

att cgc cag cct gac ggt act atc gcc ttt gtg gtc gat ttt acc ggc 2315
Ile Arg Gln Pro Asp Gly Thr Ile Ala Phe Val Val Asp Phe Thr Gly
420 425 430

gct gag atg aaa aaa ctg cca gag gat acc ccg gtc aca gcg caa acc 2363
Ala Glu Met Lys Lys Leu Pro Glu Asp Thr Pro Val Thr Ala Gln Thr
435 440 445

agc att ggt gat aat ggt gag ata gtt gaa agc acg gtg cgt tat aac 2411
Ser Ile Gly Asp Asn Gly Glu Ile Val Glu Ser Thr Val Arg Tyr Asn
450 455 460 465

ccg gtt acc aaa ggc tgg cgt ctg gtg atg cgt gtg aaa gtg aaa gat 2459
Pro Val Thr Lys Gly Trp Arg Leu Val Met Arg Val Lys Val Lys Asp
470 475 480

gcc aag aaa acc act gaa atg cgt gct gcg ctg gtg aat gcc gat cag 2507
Ala Lys Lys Thr Thr Glu Met Arg Ala Ala Leu Val Asn Ala Asp Gln
485 490 495

acg ttg agt gaa acc tgg agc tac cag tta cct gcc aat gaa 2549
Thr Leu Ser Glu Thr Trp Ser Tyr Gln Leu Pro Ala Asn Glu
500 505 510

taagacaact gactacattg acgcaatgcc catcgccgca agcgagaaaag cggcattgcc 2609

gaagactgat atccgcgccc ttcattcaggc gctggatgcc gaacaccgca cctgggcgcg 2669

ggaggatgac tccccgcaag gctcggtaaa ggcgcgtctg gaacaagcct ggccagattc 2729

acttgctgat ggacagttaa ttaaagacga cgaagggcgcg gatcagctaa aggcatgcc 2789

agaagtaaaa cgctcctcga tgtttcccga cccgtggcgt accaaccggt taggccgttt 2849

ctgggatcgc ctgcgtggac gcgatgtgac gccgcgctat ctggctcgtt tgaccaaaga 2909

agagcaggag agtgagcaaa agtggcgtag cgtcggtacc atccgccgtt acattctgtt 2969

gatcctgacg ctgcgcgcaaa ctgttgtcgc gacctggtat atgaagacca ttcttcctta 3029

```

```

tcaggggtgg gcgctgatta atcctatgga tatggttggg caggatgtgt gggtttcctt 3089
tatgcagctt ctgccttata tgctgcaaac cggtatcctg atcctctttg cggtactgtt 3149
ctggtgggtg tccgccgat tctggaccgg cgttgatggg cttcctgcaa ctgcttattg 3209
gtcgcgataa atacagtata tctgcgtcaa cagttggcga tgaaccatta aaccgggagc 3269
atcgcacggc gttgatcatg cctatctgta acgaagacgt gaaccgtgtt tttgctggct 3329
tgctgcaaac gtgggaatca gtaaaagcca ccgggaatgc caaacatttt gatgtctaca 3389
ttcttagtga cagttataac ccggatatct gcgtcgaga gcaaaaagcc tggatggagc 3449
ttatcgctga agtcggtggc gaaggtcaga ttttctatcg ccgccgccgc cgtcgctga 3509
agcgtaaaag cggtaatatc gatgacttct gccgtcgctg gggcagccag tacagctaca 3569
tggtggtgct ggatgctgac tcggtaatga ccggtgattg tttgtgcggc ctggtgcgcc 3629
tgatggaagc caaccgaac gccgggatca ttcagtcgtc gccgaaagcg tccggcatgg 3689
atacgctgta tgcgcgctgt cagcagttcg cgaccgcgt gtatgggcca ctgtttacag 3749
ccggtttgca cttctggcaa cttggcgagt cgcactactg ggggcataac gcgattatcc 3809
gcgtgaaacc gtttatcgag cactgtgcac tggctccgct gccgggcaa ggttcttttg 3869
ccggttcaat cctgtcacat gacttcgtgg aagcggcgtt gatgcgccgt gcaggttggg 3929
gggtctggat tgcttacgat ctcccgggtt cttatgaaga attaccgcct aacttgcttg 3989
atgagctaaa acgtgaccgc cgctggtgcc acggtaacct gatgaacttc cgtctgttcc 4049
tggtgaaggg tatgcacccg gttcacctg cggtgttcc tgcgggcgtg atgtcttacc 4109
tctccgctcc gctgtggttt atgttctctg cgctctctac tgcattgcag gtagtacatg 4169
cgttgaccga accgcaatac ttctgcaac cacggcagtt gttcccgta tggccgcagt 4229
ggcgtcctga gctggcgatt gcactttttg cttcgaccat ggtgctgttg ttctgcca 4289
agctattgag cattttgctt atctggtgca aaggaacgaa agaa 4333

```

<210> 2

<211> 511

<212> PRT

<213> Escherichia coli

<400> 2

Met Met Lys Met Arg Trp Leu Ser Ala Ala Val Met Leu Thr Leu Tyr  
 1 5 10 15  
 Thr Ser Ser Ser Trp Ala Phe Ser Ile Asp Asp Val Ala Lys Gln Ala  
 20 25 30  
 Gln Ser Leu Ala Gly Lys Gly Tyr Glu Ala Pro Lys Ser Asn Leu Pro  
 35 40 45  
 Ser Val Phe Arg Asp Met Lys Tyr Ala Asp Tyr Gln Gln Ile Gln Phe  
 50 55 60  
 Asn His Asp Lys Ala Tyr Trp Asn Asn Leu Lys Thr Pro Phe Lys Leu  
 65 70 75 80  
 Glu Phe Tyr His Gln Gly Met Tyr Phe Asp Thr Pro Val Lys Ile Asn  
 85 90 95  
 Glu Val Thr Ala Thr Ala Val Lys Arg Ile Lys Tyr Ser Pro Asp Tyr  
 100 105 110  
 Phe Thr Phe Gly Asp Val Gln His Asp Lys Asp Thr Val Lys Asp Leu  
 115 120 125  
 Gly Phe Ala Gly Phe Lys Val Leu Tyr Pro Ile Asn Ser Lys Asp Lys  
 130 135 140  
 Asn Asp Glu Ile Val Ser Met Leu Gly Ala Ser Tyr Phe Arg Val Ile  
 145 150 155 160  
 Gly Ala Gly Gln Val Tyr Gly Leu Ser Ala Arg Gly Leu Ala Ile Asp  
 165 170 175  
 Thr Ala Leu Pro Ser Gly Glu Glu Phe Pro Arg Phe Lys Glu Phe Trp  
 180 185 190  
 Ile Glu Arg Pro Lys Pro Thr Asp Lys Arg Leu Thr Ile Tyr Ala Leu  
 195 200 205  
 Leu Asp Ser Pro Arg Ala Thr Gly Ala Tyr Lys Phe Val Val Met Pro  
 210 215 220  
 Gly Arg Asp Thr Val Val Asp Val Gln Ser Lys Ile Tyr Leu Arg Asp  
 225 230 235 240  
 Lys Val Gly Lys Leu Gly Val Ala Pro Leu Thr Ser Met Phe Leu Phe  
 245 250 255  
 Gly Pro Asn Gln Pro Ser Pro Ala Asn Asn Tyr Arg Pro Glu Leu His  
 260 265 270

Asp Ser Asn Gly Leu Ser Ile His Ala Gly Asn Gly Glu Trp Ile Trp  
 275 280 285  
 Arg Pro Leu Asn Asn Pro Lys His Leu Ala Val Ser Ser Phe Ser Met  
 290 295 300  
 Glu Asn Pro Gln Gly Phe Gly Leu Leu Gln Arg Gly Arg Asp Phe Ser  
 305 310 315 320  
 Arg Phe Glu Asp Leu Asp Asp Arg Tyr Asp Leu Arg Pro Ser Ala Trp  
 325 330 335  
 Val Thr Pro Lys Gly Glu Trp Gly Lys Gly Ser Val Glu Leu Val Glu  
 340 345 350  
 Ile Pro Thr Asn Asp Glu Thr Asn Asp Asn Ile Val Ala Tyr Trp Thr  
 355 360 365  
 Pro Asp Gln Leu Pro Glu Pro Gly Lys Glu Met Asn Phe Lys Tyr Thr  
 370 375 380  
 Ile Thr Phe Ser Arg Asp Glu Asp Lys Leu His Ala Pro Asp Asn Ala  
 385 390 395 400  
 Trp Val Gln Gln Thr Arg Arg Ser Thr Gly Asp Val Lys Gln Ser Asn  
 405 410 415  
 Leu Ile Arg Gln Pro Asp Gly Thr Ile Ala Phe Val Val Asp Phe Thr  
 420 425 430  
 Gly Ala Glu Met Lys Lys Leu Pro Glu Asp Thr Pro Val Thr Ala Gln  
 435 440 445  
 Thr Ser Ile Gly Asp Asn Gly Glu Ile Val Glu Ser Thr Val Arg Tyr  
 450 455 460  
 Asn Pro Val Thr Lys Gly Trp Arg Leu Val Met Arg Val Lys Val Lys  
 465 470 475 480  
 Asp Ala Lys Lys Thr Thr Glu Met Arg Ala Ala Leu Val Asn Ala Asp  
 485 490 495  
 Gln Thr Leu Ser Glu Thr Trp Ser Tyr Gln Leu Pro Ala Asn Glu  
 500 505 510

<210> 3

<211> 574

<212> DNA

<213> Escherichia coli

&lt;400&gt; 3

```

ttcgttgatc ctgtcaccgt ttgttcggtt atttccagcc gtgccaccgt tggctctgca 60
accaaacgct ggaaactgtt ccctgatccc ggaagagtat tcaccgccgc aggtgctggt 120
tgataccgat cggttccttg agatgaatcg tcaatgctcc cttgatgatg gttttatgca 180
cgcggtgttt aaccgcgtcat ttaacgctct ggcaaccgca atggcgaccg cgcgtcaccg 240
cgccagcaag gtgctggaaa tcgcccgtga ccgccacgtt gaacaggcgc tgaacgagac 300
gccagagaag ctgaatcgcg atcgtcgcct ggtgctgcta agcgatccgg tgacgatggc 360
ccgtctgcat ttccgcgtct ggaattcccc ggagagatat tcttcatggg tgagttatta 420
cgaagggata aagctcaatc cactggcatt gcgtaaaccg gatgcggctt cgcaataaaa 480
acgtagtgtc ctgatgcgct acgcttatca ggcctacatc gttcctgcaa tttattgatt 540
ttgcaagatt ttgtaggctc gataaggcgt tcac 574

```

&lt;210&gt; 4

&lt;211&gt; 1478

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (25)..(1449)

&lt;400&gt; 4

```

gggataatgc ctgagggggcc tgta atg cgt atc ggc atg cgg ttg ttg ctg 51
                               Met Arg Ile Gly Met Arg Leu Leu Leu
                               1             5

ggc tat ttt tta ctg gtg gcg gtg gcg gcc tgg ttc gta ctg gct att 99
Gly Tyr Phe Leu Leu Val Ala Val Ala Ala Trp Phe Val Leu Ala Ile
10             15             20             25

ttt gtc aaa gaa gtt aaa ccg ggc gtg cga aga gca acc gag ggg acg 147
Phe Val Lys Glu Val Lys Pro Gly Val Arg Arg Ala Thr Glu Gly Thr
30             35             40

tta atc gac acc gca acg ttg ctg gcg gag ctg gcg cgt ccc gat ttg 195
Leu Ile Asp Thr Ala Thr Leu Leu Ala Glu Leu Ala Arg Pro Asp Leu
45             50             55

ctc tct ggg gac cca acg cat ggg caa ctg gcg cag gcg ttt aat cag 243
Leu Ser Gly Asp Pro Thr His Gly Gln Leu Ala Gln Ala Phe Asn Gln
60             65             70

cta caa cat cgc ccg ttt cgc gcc aat atc ggt ggc att aac aaa gtg 291
Leu Gln His Arg Pro Phe Arg Ala Asn Ile Gly Gly Ile Asn Lys Val
75             80             85

cgc aac gaa tat cat gtc tat atg acc gat gcg cag ggc aaa gta ttg 339
Arg Asn Glu Tyr His Val Tyr Met Thr Asp Ala Gln Gly Lys Val Leu
90             95             100             105

```



ttc gat tcg gca aat aaa gcc gtt gga cag gat tat tcg cgc tgg aat	387
Phe Asp Ser Ala Asn Lys Ala Val Gly Gln Asp Tyr Ser Arg Trp Asn	
110 115 120	
gac gtc tgg cta acg ttg cgt ggt cag tat ggt gcg cgc agc acg ttg	435
Asp Val Trp Leu Thr Leu Arg Gly Gln Tyr Gly Ala Arg Ser Thr Leu	
125 130 135	
caa aat cct gcc gat ccc gaa agt tct gtg atg tat gtt gcc gcg ccg	483
Gln Asn Pro Ala Asp Pro Glu Ser Ser Val Met Tyr Val Ala Ala Pro	
140 145 150	
att atg gac ggc tcg cgg ctt att ggc gtt ttg agc gta ggc aaa ccg	531
Ile Met Asp Gly Ser Arg Leu Ile Gly Val Leu Ser Val Gly Lys Pro	
155 160 165	
aac gcg gcg atg gct ccg gtc att aag cgt agc gag cgg cga att tta	579
Asn Ala Ala Met Ala Pro Val Ile Lys Arg Ser Glu Arg Arg Ile Leu	
170 175 180 185	
tgg gcc agc gcc att ttg ttg ggg att gca ctg gtg att ggc gca ggc	627
Trp Ala Ser Ala Ile Leu Leu Gly Ile Ala Leu Val Ile Gly Ala Gly	
190 195 200	
atg gtt tgg tgg atc aac cgc tct att gcc agg ctc act cgc tat gct	675
Met Val Trp Trp Ile Asn Arg Ser Ile Ala Arg Leu Thr Arg Tyr Ala	
205 210 215	
gat tcc gtc act gac aat aag ccc gtt cct ctc ccc gat ctc ggt agt	723
Asp Ser Val Thr Asp Asn Lys Pro Val Pro Leu Pro Asp Leu Gly Ser	
220 225 230	
agc gag ttg cgt aaa ctc gcg cag gcg ctg gaa agt atg cgc gtg aag	771
Ser Glu Leu Arg Lys Leu Ala Gln Ala Leu Glu Ser Met Arg Val Lys	
235 240 245	
ctg gaa ggg aaa aac tat att gag cag tat gtt tat gcg tta act cat	819
Leu Glu Gly Lys Asn Tyr Ile Glu Gln Tyr Val Tyr Ala Leu Thr His	
250 255 260 265	
gag cta aaa agc cca ctg gcg gcg att cgt ggc gcg gcg gaa att tta	867
Glu Leu Lys Ser Pro Leu Ala Ala Ile Arg Gly Ala Ala Glu Ile Leu	
270 275 280	
cgc gaa ggt ccg ccg ccg gaa gtg gtg gct cgt ttt acc gac aac att	915
Arg Glu Gly Pro Pro Pro Glu Val Val Ala Arg Phe Thr Asp Asn Ile	
285 290 295	
ctg acg caa aat gcg cga atg cag gca ctg gtg gaa acg tta cta cgc	963
Leu Thr Gln Asn Ala Arg Met Gln Ala Leu Val Glu Thr Leu Leu Arg	
300 305 310	

```

cag gca aga ctg gag aat cgt cag gaa gtc gtt ctg act gct gtt gat 1011
Gln Ala Arg Leu Glu Asn Arg Gln Glu Val Val Leu Thr Ala Val Asp
    315                320                325

gtg gcg gca tta ttt cgc cgc gtc agc gaa gcg cgc acc gtg cag ttg 1059
Val Ala Ala Leu Phe Arg Arg Val Ser Glu Ala Arg Thr Val Gln Leu
    330                335                340                345

gca gaa aaa aac atc act ttg cat gtt atg cct act gag gtt aac gtt 1107
Ala Glu Lys Asn Ile Thr Leu His Val Met Pro Thr Glu Val Asn Val
                350                355                360

gct tct gaa ccg gcg tta ctg gag cag gcg ctg ggg aat tta ctg gat 1155
Ala Ser Glu Pro Ala Leu Leu Glu Gln Ala Leu Gly Asn Leu Leu Asp
                365                370                375

aac gcc atc gat ttt act ccc gag agc ggt tgc ata acg cta agc gcc 1203
Asn Ala Ile Asp Phe Thr Pro Glu Ser Gly Cys Ile Thr Leu Ser Ala
                380                385                390

gaa gtg gat cag gaa tac gtc acc ctt aag gtg ctg gat acc ggt agt 1251
Glu Val Asp Gln Glu Tyr Val Thr Leu Lys Val Leu Asp Thr Gly Ser
    395                400                405

ggg att cct gac tac gcg ctg tca cgt att ttt gaa cgc ttt tac tct 1299
Gly Ile Pro Asp Tyr Ala Leu Ser Arg Ile Phe Glu Arg Phe Tyr Ser
    410                415                420                425

ttg ccg cgt gca aat ggg caa aaa agc agc ggt ctg ggg ttg gcg ttt 1347
Leu Pro Arg Ala Asn Gly Gln Lys Ser Ser Gly Leu Gly Leu Ala Phe
                430                435                440

gtc agt gag gtc gcc cgt ttg ttt aac ggc gaa gtc acg ctg cgc aac 1395
Val Ser Glu Val Ala Arg Leu Phe Asn Gly Glu Val Thr Leu Arg Asn
                445                450                455

gtg cag gaa ggt ggc gtg ctg gcc tcg ctt cga ctt cac cgt cac ttc 1443
Val Gln Glu Gly Gly Val Leu Ala Ser Leu Arg Leu His Arg His Phe
    460                465                470

aca tag cttcaaattc ttccacata gtcttcgta 1478
Thr
    475

```

&lt;210&gt; 5

&lt;211&gt; 474

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 5

Met	Arg	Ile	Gly	Met	Arg	Leu	Leu	Leu	Gly	Tyr	Phe	Leu	Leu	Val	Ala	1	5	10	15
Val	Ala	Ala	Trp	Phe	Val	Leu	Ala	Ile	Phe	Val	Lys	Glu	Val	Lys	Pro	20	25	30	
Gly	Val	Arg	Arg	Ala	Thr	Glu	Gly	Thr	Leu	Ile	Asp	Thr	Ala	Thr	Leu	35	40	45	
Leu	Ala	Glu	Leu	Ala	Arg	Pro	Asp	Leu	Leu	Ser	Gly	Asp	Pro	Thr	His	50	55	60	
Gly	Gln	Leu	Ala	Gln	Ala	Phe	Asn	Gln	Leu	Gln	His	Arg	Pro	Phe	Arg	65	70	75	80
Ala	Asn	Ile	Gly	Gly	Ile	Asn	Lys	Val	Arg	Asn	Glu	Tyr	His	Val	Tyr	85	90	95	
Met	Thr	Asp	Ala	Gln	Gly	Lys	Val	Leu	Phe	Asp	Ser	Ala	Asn	Lys	Ala	100	105	110	
Val	Gly	Gln	Asp	Tyr	Ser	Arg	Trp	Asn	Asp	Val	Trp	Leu	Thr	Leu	Arg	115	120	125	
Gly	Gln	Tyr	Gly	Ala	Arg	Ser	Thr	Leu	Gln	Asn	Pro	Ala	Asp	Pro	Glu	130	135	140	
Ser	Ser	Val	Met	Tyr	Val	Ala	Ala	Pro	Ile	Met	Asp	Gly	Ser	Arg	Leu	145	150	155	160
Ile	Gly	Val	Leu	Ser	Val	Gly	Lys	Pro	Asn	Ala	Ala	Met	Ala	Pro	Val	165	170	175	
Ile	Lys	Arg	Ser	Glu	Arg	Arg	Ile	Leu	Trp	Ala	Ser	Ala	Ile	Leu	Leu	180	185	190	
Gly	Ile	Ala	Leu	Val	Ile	Gly	Ala	Gly	Met	Val	Trp	Trp	Ile	Asn	Arg	195	200	205	
Ser	Ile	Ala	Arg	Leu	Thr	Arg	Tyr	Ala	Asp	Ser	Val	Thr	Asp	Asn	Lys	210	215	220	
Pro	Val	Pro	Leu	Pro	Asp	Leu	Gly	Ser	Ser	Glu	Leu	Arg	Lys	Leu	Ala	225	230	235	240
Gln	Ala	Leu	Glu	Ser	Met	Arg	Val	Lys	Leu	Glu	Gly	Lys	Asn	Tyr	Ile	245	250	255	
Glu	Gln	Tyr	Val	Tyr	Ala	Leu	Thr	His	Glu	Leu	Lys	Ser	Pro	Leu	Ala	260	265	270	

Ala Ile Arg Gly Ala Ala Glu Ile Leu Arg Glu Gly Pro Pro Pro Glu  
           275                          280                          285  
 Val Val Ala Arg Phe Thr Asp Asn Ile Leu Thr Gln Asn Ala Arg Met  
           290                          295                          300  
 Gln Ala Leu Val Glu Thr Leu Leu Arg Gln Ala Arg Leu Glu Asn Arg  
 305                          310                          315                          320  
 Gln Glu Val Val Leu Thr Ala Val Asp Val Ala Ala Leu Phe Arg Arg  
                           325                          330                          335  
 Val Ser Glu Ala Arg Thr Val Gln Leu Ala Glu Lys Asn Ile Thr Leu  
                           340                          345                          350  
 His Val Met Pro Thr Glu Val Asn Val Ala Ser Glu Pro Ala Leu Leu  
           355                          360                          365  
 Glu Gln Ala Leu Gly Asn Leu Leu Asp Asn Ala Ile Asp Phe Thr Pro  
           370                          375                          380  
 Glu Ser Gly Cys Ile Thr Leu Ser Ala Glu Val Asp Gln Glu Tyr Val  
 385                          390                          395                          400  
 Thr Leu Lys Val Leu Asp Thr Gly Ser Gly Ile Pro Asp Tyr Ala Leu  
                           405                          410                          415  
 Ser Arg Ile Phe Glu Arg Phe Tyr Ser Leu Pro Arg Ala Asn Gly Gln  
                           420                          425                          430  
 Lys Ser Ser Gly Leu Gly Leu Ala Phe Val Ser Glu Val Ala Arg Leu  
           435                          440                          445  
 Phe Asn Gly Glu Val Thr Leu Arg Asn Val Gln Glu Gly Gly Val Leu  
           450                          455                          460  
 Ala Ser Leu Arg Leu His Arg His Phe Thr  
 465                          470

<210> 6

<211> 128

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(126)

<400> 6

atg aaa ggt cgc ctg tta gat gct gtc ccg ctc agt tcc cta acg ggc 48  
 Met Lys Gly Arg Leu Leu Asp Ala Val Pro Leu Ser Ser Leu Thr Gly  
 1 5 10 15

gtt ggc gca gcg ctt agt aac aag ctg gcg aaa atc aac ctg cat acc 96  
 Val Gly Ala Ala Leu Ser Asn Lys Leu Ala Lys Ile Asn Leu His Thr  
 20 25 30

gta cag gat tta ctc tta cac ctt cct ctg cg 128  
 Val Gln Asp Leu Leu Leu His Leu Pro Leu  
 35 40

<210> 7  
 <211> 42  
 <212> PRT  
 <213> Escherichia coli

<400> 7  
 Met Lys Gly Arg Leu Leu Asp Ala Val Pro Leu Ser Ser Leu Thr Gly  
 1 5 10 15

Val Gly Ala Ala Leu Ser Asn Lys Leu Ala Lys Ile Asn Leu His Thr  
 20 25 30

Val Gln Asp Leu Leu Leu His Leu Pro Leu  
 35 40

<210> 8  
 <211> 1174  
 <212> DNA  
 <213> Escherichia coli

<220>  
 <221> CDS  
 <222> (121)..(837)

<400> 8  
 agatgcacga tcgagtaggc cggataaggc gtttacgccg catccagcat ggaaaacgcg 60  
 cactttgtta tcaatctggg gccagcaaat gctggcctga tttgttcttg agggaagact 120

atg atg cgc aaa atg ctg ctg gcg gca gca ctt tca gtg acg gca atg 168  
 Met Met Arg Lys Met Leu Leu Ala Ala Ala Leu Ser Val Thr Ala Met  
 1 5 10 15

acc gct cac gcc gac tac cag tgc agc gtc acg ccg cgt gac gat gtg 216  
 Thr Ala His Ala Asp Tyr Gln Cys Ser Val Thr Pro Arg Asp Asp Val  
 20 25 30

att gtc agc ccg caa acc gtg cag gtg aag ggc gaa aac ggc aat ctg	264
Ile Val Ser Pro Gln Thr Val Gln Val Lys Gly Glu Asn Gly Asn Leu	
35 40 45	
gtg atc acg cca gac ggc aac gtg atg tat aac ggt aag caa tat tcc	312
Val Ile Thr Pro Asp Gly Asn Val Met Tyr Asn Gly Lys Gln Tyr Ser	
50 55 60	
ctg aat gcc gcc cag cgc gag cag gcg aag gat tat cag gct gaa cta	360
Leu Asn Ala Ala Gln Arg Glu Gln Ala Lys Asp Tyr Gln Ala Glu Leu	
65 70 75 80	
cgt agc acc ctg ccg tgg att gat gga ggc gcg aaa agc cgc gtc gag	408
Arg Ser Thr Leu Pro Trp Ile Asp Gly Gly Ala Lys Ser Arg Val Glu	
85 90 95	
aaa gct cgt att gcg ctg gat aaa att atc gtt cag gag atg ggc gaa	456
Lys Ala Arg Ile Ala Leu Asp Lys Ile Ile Val Gln Glu Met Gly Glu	
100 105 110	
agc agc aaa atg cgc agc cgt ctg acc aaa ctt gat gcg cag ctg aaa	504
Ser Ser Lys Met Arg Ser Arg Leu Thr Lys Leu Asp Ala Gln Leu Lys	
115 120 125	
gag cag atg aac cgc att atc gaa acg cgc agc gat ggc ctg acg ttt	552
Glu Gln Met Asn Arg Ile Ile Glu Thr Arg Ser Asp Gly Leu Thr Phe	
130 135 140	
cac tat aaa gcc att gat cag gtt cgt gcc gaa ggc cag caa tta gtg	600
His Tyr Lys Ala Ile Asp Gln Val Arg Ala Glu Gly Gln Gln Leu Val	
145 150 155 160	
aat cag gca atg ggc gga att tta cag gac agc att aat gaa atg ggc	648
Asn Gln Ala Met Gly Gly Ile Leu Gln Asp Ser Ile Asn Glu Met Gly	
165 170 175	
gcg aaa gcg gtg ctg aaa agc ggc ggt aac cca tta cag aac gtg ctg	696
Ala Lys Ala Val Leu Lys Ser Gly Gly Asn Pro Leu Gln Asn Val Leu	
180 185 190	
gga agc ctg ggc ggc ctg caa tcc tca atc caa acc gag tgg aaa aag	744
Gly Ser Leu Gly Gly Leu Gln Ser Ser Ile Gln Thr Glu Trp Lys Lys	
195 200 205	
cag gaa aaa gat ttc cag cag ttt ggc aaa gat gtt tgt agc cgc gtt	792
Gln Glu Lys Asp Phe Gln Gln Phe Gly Lys Asp Val Cys Ser Arg Val	
210 215 220	
gtg act ctg gaa gat agc cgc aaa gcc ctg gtc ggg aat tta aaa	837
Val Thr Leu Glu Asp Ser Arg Lys Ala Leu Val Gly Asn Leu Lys	
225 230 235	

taatcctcta ttttaagacg gcataatact tttttatgcc gtttaattct tcgttttggt 897  
 acctgcctct aactttgtaa gggcgaattc tgcagatata catcacactg gcggccgctc 957  
 gagcatgcat ctagagggcc caattcgccc tatagtgagt cgtattacaa ttcactggcc 1017  
 gtcgttttac aaccgtcgtg actgggaaaa ccctggcggt acccaactta atcgccctgc 1077  
 agcacatccc cctttcgcca gctggcgtaa tagcgaaaag gcccgaccg atcgcccttc 1137  
 caacagttgc gcacctgatg gccaatggac gcgcctg 1174

<210> 9

<211> 239

<212> PRT

<213> Escherichia coli

<400> 9

Met	Met	Arg	Lys	Met	Leu	Leu	Ala	Ala	Ala	Leu	Ser	Val	Thr	Ala	Met
1				5					10					15	
Thr	Ala	His	Ala	Asp	Tyr	Gln	Cys	Ser	Val	Thr	Pro	Arg	Asp	Asp	Val
			20					25					30		
Ile	Val	Ser	Pro	Gln	Thr	Val	Gln	Val	Lys	Gly	Glu	Asn	Gly	Asn	Leu
		35					40					45			
Val	Ile	Thr	Pro	Asp	Gly	Asn	Val	Met	Tyr	Asn	Gly	Lys	Gln	Tyr	Ser
	50					55				60					
Leu	Asn	Ala	Ala	Gln	Arg	Glu	Gln	Ala	Lys	Asp	Tyr	Gln	Ala	Glu	Leu
65					70					75					80
Arg	Ser	Thr	Leu	Pro	Trp	Ile	Asp	Gly	Gly	Ala	Lys	Ser	Arg	Val	Glu
				85					90					95	
Lys	Ala	Arg	Ile	Ala	Leu	Asp	Lys	Ile	Ile	Val	Gln	Glu	Met	Gly	Glu
			100					105					110		
Ser	Ser	Lys	Met	Arg	Ser	Arg	Leu	Thr	Lys	Leu	Asp	Ala	Gln	Leu	Lys
		115					120					125			
Glu	Gln	Met	Asn	Arg	Ile	Ile	Glu	Thr	Arg	Ser	Asp	Gly	Leu	Thr	Phe
	130					135					140				
His	Tyr	Lys	Ala	Ile	Asp	Gln	Val	Arg	Ala	Glu	Gly	Gln	Gln	Leu	Val
145					150					155					160
Asn	Gln	Ala	Met	Gly	Gly	Ile	Leu	Gln	Asp	Ser	Ile	Asn	Glu	Met	Gly
			165					170					175		

Ala Lys Ala Val Leu Lys Ser Gly Gly Asn Pro Leu Gln Asn Val Leu  
                   180                  185                  190

Gly Ser Leu Gly Gly Leu Gln Ser Ser Ile Gln Thr Glu Trp Lys Lys  
                   195                  200                  205

Gln Glu Lys Asp Phe Gln Gln Phe Gly Lys Asp Val Cys Ser Arg Val  
                   210                  215                  220

Val Thr Leu Glu Asp Ser Arg Lys Ala Leu Val Gly Asn Leu Lys  
                   225                  230                  235

<210> 10  
 <211> 3406  
 <212> DNA  
 <213> Escherichia coli

<220>  
 <221> CDS  
 <222> (1007) .. (1276)

<220>  
 <221> CDS  
 <222> (1280) .. (1792)

<220>  
 <221> CDS  
 <222> (1798) .. (2574)

<220>  
 <221> CDS  
 <222> (2604) .. (3398)

<400> 10  
 gatgatggtg atggagcgta ttacgcat tccggtgtct gatgttgca cgctggagaa 60  
 aaacggcacc aacatgaaat tgctggcgga acgcggcgtg caggtgttct tcactcaggt 120  
 ctttcgac agctttttcc atgctgatat gcacctggc aacatcttcg taagctatga 180  
 acacccggaa aacccgaaat atatcgcat tgattgcggg attgttggct cgctaaacaa 240  
 agaagataaa cgctatctgg cggaaaactt tatcgcttc tttaatcgcg actatcgcaa 300  
 agtggcagag ctacacgtcg attctggttg ggtgccacca gataccaacg ttgaagagtt 360  
 cgaatttgcc attcgtacgg tctgtgaacc tatctttgag aaaccgctgg ccgaaatttc 420  
 gtttgacat gtactgttaa atctgtttaa tacggcgcgt cgcttcaata tggaagtgca 480



```

gccgcaactg gtgttactcc agaaaaccct gctctacgtc gaaggggtag gacgccagct 540
ttatccgcaa ctcgatttat ggaaaacggc gaagcctttc ctggagtcgt ggattaaaga 600
tcaggtcggt attcctgcgc tggtagagagc atttaaagaa aaagcgccgt tctgggtcga 660
aaaaatgcca gaactgcctg aactgggttta cgacagtttg cgccagggca agtatttaca 720
gcatagtgtt ggtaagattg cccgcgagct tcagtcaaat catgtacgtc agggacaatt 780
cgcgttattt tctcgggaatt ggcgctacgt tagtatttaa gtggcacatt cttgttggtc 840
agccgacctg aatgggggct gatgcccggc tggttaatgg caggtggtct gatcgccctgg 900
tttgtccggt tggcgcaaaa cacgctgatt ttttcatcgc tcaaggcggg ccgtgtaacg 960
tataatgcgg ctttgtttta tcatcatcta ccacagagga acatgt atg ggt ggt 1015
                                   Met Gly Gly
                                   1

atc agt att tgg cag tta ttg att att gcc gtc atc gtt gta ctg ctt 1063
Ile Ser Ile Trp Gln Leu Leu Ile Ile Ala Val Ile Val Val Leu Leu
      5                10                15

ttt ggc acc aaa aag ctc ggc tcc atc ggt tcc gat ctt ggt gcg tcg 1111
Phe Gly Thr Lys Lys Leu Gly Ser Ile Gly Ser Asp Leu Gly Ala Ser
  20                25                30                35

atc aaa ggc ttt aaa aaa gca atg agc gat gat gaa cca aag cag gat 1159
Ile Lys Gly Phe Lys Lys Ala Met Ser Asp Asp Glu Pro Lys Gln Asp
                40                45                50

aaa acc agc cag gat gct gat ttt act gcg aaa act atc gcc gat aag 1207
Lys Thr Ser Gln Asp Ala Asp Phe Thr Ala Lys Thr Ile Ala Asp Lys
      55                60                65

cag gcg gat acg aat cag gaa cag gct aaa ata gaa gac gcg aag cgc 1255
Gln Ala Asp Thr Asn Gln Glu Gln Ala Lys Ile Glu Asp Ala Lys Arg
      70                75                80

cac gat aaa gag cag gtg taa tct gtg ttt gat atc ggt ttt agc gaa 1303
His Asp Lys Glu Gln Val          Val Phe Asp Ile Gly Phe Ser Glu
      85                90                95

ctg cta ttg gtg ttc atc atc ggc ctc gtc gtt ctg ggg ccg caa cga 1351
Leu Leu Leu Val Phe Ile Ile Gly Leu Val Val Leu Gly Pro Gln Arg
    100                105                110

ctg cct gtg gcg gta aaa acg gta gcg ggc tgg att cgc gcg ttg cgt 1399
Leu Pro Val Ala Val Lys Thr Val Ala Gly Trp Ile Arg Ala Leu Arg
    115                120                125                130

```

tca ctg gcg aca acg gtg cag aac gaa ctg acc cag gag tta aaa ctc	1447
Ser Leu Ala Thr Thr Val Gln Asn Glu Leu Thr Gln Glu Leu Lys Leu	
135 140 145	
cag gag ttt cag gac agt ctg aaa aag gtt gaa aag gcg agc ctc act	1495
Gln Glu Phe Gln Asp Ser Leu Lys Lys Val Glu Lys Ala Ser Leu Thr	
150 155 160	
aac ctg acg ccc gaa ctg aaa gcg tcg atg gat gaa tta cgc cag gct	1543
Asn Leu Thr Pro Glu Leu Lys Ala Ser Met Asp Glu Leu Arg Gln Ala	
165 170 175	
gcg gag tcg atg aaa cgt tcc tac gtt gca aac gat cct gaa aag gcg	1591
Ala Glu Ser Met Lys Arg Ser Tyr Val Ala Asn Asp Pro Glu Lys Ala	
180 185 190	
agc gat gaa gcg cac acc atc cat aac ccg gtg gtg aaa gac aat gaa	1639
Ser Asp Glu Ala His Thr Ile His Asn Pro Val Val Lys Asp Asn Glu	
195 200 205 210	
act gcg cat gaa ggc gta acg cct gct gct gca caa acg cag gcc agt	1687
Thr Ala His Glu Gly Val Thr Pro Ala Ala Ala Gln Thr Gln Ala Ser	
215 220 225	
tcg ccg gaa cag aag cca gaa acc acg cca gag ccg gtg gta aaa cct	1735
Ser Pro Glu Gln Lys Pro Glu Thr Thr Pro Glu Pro Val Val Lys Pro	
230 235 240	
gct gcg gac gct gaa ccg aaa acc gct gca cct tcc cct tcg tcg agt	1783
Ala Ala Asp Ala Glu Pro Lys Thr Ala Ala Pro Ser Pro Ser Ser Ser	
245 250 255	
gat aaa ccg taaac atg tct gta gaa gat act caa ccg ctt atc acg cat	1833
Asp Lys Pro Met Ser Val Glu Asp Thr Gln Pro Leu Ile Thr His	
260 265 270	
ctg att gag ctg cgt aag cgt ctg ctg aac tgc att atc tcg gtg atc	1881
Leu Ile Glu Leu Arg Lys Arg Leu Leu Asn Cys Ile Ile Ser Val Ile	
275 280 285	
gtg ata ttc ctg tgt ctg gtc tat ttc gcc aat gac atc tat cac ctg	1929
Val Ile Phe Leu Cys Leu Val Tyr Phe Ala Asn Asp Ile Tyr His Leu	
290 295 300 305	
gta tcc gcg cca ctg atc aag cag ttg ccg caa ggt tca acg atg atc	1977
Val Ser Ala Pro Leu Ile Lys Gln Leu Pro Gln Gly Ser Thr Met Ile	
310 315 320	
gcc acc gac gtg gcc tcg ccg ttc ttt acg ccg atc aag ctg acc ttt	2025
Ala Thr Asp Val Ala Ser Pro Phe Phe Thr Pro Ile Lys Leu Thr Phe	
325 330 335	

atg gtg tcg ctg att ctg tca gcg ccg gtg att ctc tat cag gtg tgg	2073
Met Val Ser Leu Ile Leu Ser Ala Pro Val Ile Leu Tyr Gln Val Trp	
340 345 350	
gcg ttt atc gcc cca gcg ctg tat aag cat gaa cgt cgc ctg gtg gtg	2121
Ala Phe Ile Ala Pro Ala Leu Tyr Lys His Glu Arg Arg Leu Val Val	
355 360 365	
ccg ctg ctg gtt tcc agc tct ctg ctg ttt tat atc ggc atg gcg ttc	2169
Pro Leu Leu Val Ser Ser Ser Leu Leu Phe Tyr Ile Gly Met Ala Phe	
370 375 380 385	
gcc tac ttt gtg gtc ttt ccg ctg gca ttt ggc ttc ctt gcc aat acc	2217
Ala Tyr Phe Val Val Phe Pro Leu Ala Phe Gly Phe Leu Ala Asn Thr	
390 395 400	
gcg ccg gaa ggg gta cag gta tcc acc gac atc gcg agc tat tta agc	2265
Ala Pro Glu Gly Val Gln Val Ser Thr Asp Ile Ala Ser Tyr Leu Ser	
405 410 415	
ttc gtt atg gcg ctg ttt atg gcg ttt ggt gtc tcc ttt gaa gtg ccg	2313
Phe Val Met Ala Leu Phe Met Ala Phe Gly Val Ser Phe Glu Val Pro	
420 425 430	
gtg gca att gtg ctg ctg tgc tgg atg ggg att acc tcg cca gaa gac	2361
Val Ala Ile Val Leu Leu Cys Trp Met Gly Ile Thr Ser Pro Glu Asp	
435 440 445	
tta cgc aaa aaa cgc ccg tat gtg ctg gtt ggt gca ttc gtt gtc ggg	2409
Leu Arg Lys Lys Arg Pro Tyr Val Leu Val Gly Ala Phe Val Val Gly	
450 455 460 465	
atg ttg ctg acg ccg ccg gat gtc ttc tcg caa acg ctg ttg gcg atc	2457
Met Leu Leu Thr Pro Pro Asp Val Phe Ser Gln Thr Leu Leu Ala Ile	
470 475 480	
cct atg tac tgc ctg ttt gaa atc ggt gtc ttc ttc tca cgc ttt tac	2505
Pro Met Tyr Cys Leu Phe Glu Ile Gly Val Phe Phe Ser Arg Phe Tyr	
485 490 495	
gtt ggt aaa ggg cga aac cgg gaa gag gaa aac gac gct gaa gca gaa	2553
Val Gly Lys Gly Arg Asn Arg Glu Glu Glu Asn Asp Ala Glu Ala Glu	
500 505 510	
agc gaa aaa act gaa gaa taa attcaaccgc ccgtcagggc gggtgtcat atg	2606
Ser Glu Lys Thr Glu Glu Met	
515 520	
gag tac agg atg ttt gat atc ggc gtt aat ttg acc agt tcg caa ttt	2654
Glu Tyr Arg Met Phe Asp Ile Gly Val Asn Leu Thr Ser Ser Gln Phe	
525 530 535	

gcg aaa gac cgt gat gat gtt gta gcg cgc gct ttt gac gcg gga gtt Ala Lys Asp Arg Asp Asp Val Val Ala Arg Ala Phe Asp Ala Gly Val 540 545 550	2702
aat ggg cta ctc atc acc ggt acc aat ctg cgt gaa agc cag cag gcg Asn Gly Leu Leu Ile Thr Gly Thr Asn Leu Arg Glu Ser Gln Gln Ala 555 560 565	2750
caa aag ctg gcg cgt cag tat tcg tcc tgt tgg tca acg gcg ggc gta Gln Lys Leu Ala Arg Gln Tyr Ser Ser Cys Trp Ser Thr Ala Gly Val 570 575 580 585	2798
cat cct cac gac agc agc cag tgg caa gct gtg act gaa gaa gcg att His Pro His Asp Ser Ser Gln Trp Gln Ala Val Thr Glu Glu Ala Ile 590 595 600	2846
att gag ctg gcc gcg cag cca gaa gtg gtg gcg att ggt gaa tgt ggt Ile Glu Leu Ala Ala Gln Pro Glu Val Val Ala Ile Gly Glu Cys Gly 605 610 615	2894
ctc gac ttt aac cgc aac ttt tcg acg ccg gaa gag cag gaa cgc gct Leu Asp Phe Asn Arg Asn Phe Ser Thr Pro Glu Glu Gln Glu Arg Ala 620 625 630	2942
ttt gtt gcc cag cta cgc att gcc gca gaa tta aac atg ccg gta ttt Phe Val Ala Gln Leu Arg Ile Ala Ala Glu Leu Asn Met Pro Val Phe 635 640 645	2990
atg cac tgt cgc gat gcc cac gag cgg ttt atg aca ttg ctg gag ccg Met His Cys Arg Asp Ala His Glu Arg Phe Met Thr Leu Leu Glu Pro 650 655 660 665	3038
tgg ctg gat aaa ctg cct ggt gcg gtt ctt cat tgc ttt acc ggc aca Trp Leu Asp Lys Leu Pro Gly Ala Val Leu His Cys Phe Thr Gly Thr 670 675 680	3086
cgc gaa gag atg cag gcg tgc gtg gcg tgt gga att tat atc ggc att Arg Glu Glu Met Gln Ala Cys Val Ala Cys Gly Ile Tyr Ile Gly Ile 685 690 695	3134
acc ggt tgg gtt tgc gat gaa cga cgc ggg ctg gag ctg cgg gaa ttg Thr Gly Trp Val Cys Asp Glu Arg Arg Gly Leu Glu Leu Arg Glu Leu 700 705 710	3182
ttg ccg ttg att ccg gcg gag aaa ttg ctg atc gaa act gat gcg ccg Leu Pro Leu Ile Pro Ala Glu Lys Leu Leu Ile Glu Thr Asp Ala Pro 715 720 725	3230
tat ctg ctc cct cgc gat ctc acg cca aag cca tca tcc cgg cgc aac Tyr Leu Leu Pro Arg Asp Leu Thr Pro Lys Pro Ser Ser Arg Arg Asn 730 735 740 745	3278

gag cca gcc cat ctg ccc cat att ttg caa cgt att gcg cac tgg cgt 3326  
 Glu Pro Ala His Leu Pro His Ile Leu Gln Arg Ile Ala His Trp Arg  
                   750                  755                  760

gga gaa gat gcc gca tgg ctg gct gcc acc acg gat gcc aat gtc aaa 3374  
 Gly Glu Asp Ala Ala Trp Leu Ala Ala Thr Thr Asp Ala Asn Val Lys  
                   765                  770                  775

aca ctg ttt ggg att gcg ttt tag agtttgcg 3406  
 Thr Leu Phe Gly Ile Ala Phe  
                   780                  785

<210> 11  
 <211> 89  
 <212> PRT  
 <213> Escherichia coli

<400> 11  
 Met Gly Gly Ile Ser Ile Trp Gln Leu Leu Ile Ile Ala Val Ile Val  
   1                  5                  10                  15

Val Leu Leu Phe Gly Thr Lys Lys Leu Gly Ser Ile Gly Ser Asp Leu  
                   20                  25                  30

Gly Ala Ser Ile Lys Gly Phe Lys Lys Ala Met Ser Asp Asp Glu Pro  
                   35                  40                  45

Lys Gln Asp Lys Thr Ser Gln Asp Ala Asp Phe Thr Ala Lys Thr Ile  
                   50                  55                  60

Ala Asp Lys Gln Ala Asp Thr Asn Gln Glu Gln Ala Lys Ile Glu Asp  
                   65                  70                  75                  80

Ala Lys Arg His Asp Lys Glu Gln Val  
                   85

<210> 12  
 <211> 171  
 <212> PRT  
 <213> Escherichia coli

<400> 12  
 Val Phe Asp Ile Gly Phe Ser Glu Leu Leu Leu Val Phe Ile Ile Gly  
   1                  5                  10                  15

Leu Val Val Leu Gly Pro Gln Arg Leu Pro Val Ala Val Lys Thr Val  
                   20                  25                  30

Ala Gly Trp Ile Arg Ala Leu Arg Ser Leu Ala Thr Thr Val Gln Asn

35	40	45
Glu Leu Thr Gln Glu Leu Lys Leu Gln Glu Phe Gln Asp Ser Leu Lys		
50	55	60
Lys Val Glu Lys Ala Ser Leu Thr Asn Leu Thr Pro Glu Leu Lys Ala		
65	70	75
Ser Met Asp Glu Leu Arg Gln Ala Ala Glu Ser Met Lys Arg Ser Tyr		
	85	90
Val Ala Asn Asp Pro Glu Lys Ala Ser Asp Glu Ala His Thr Ile His		
	100	105
Asn Pro Val Val Lys Asp Asn Glu Thr Ala His Glu Gly Val Thr Pro		
	115	120
Ala Ala Ala Gln Thr Gln Ala Ser Ser Pro Glu Gln Lys Pro Glu Thr		
	130	135
Thr Pro Glu Pro Val Val Lys Pro Ala Ala Asp Ala Glu Pro Lys Thr		
	145	150
Ala Ala Pro Ser Pro Ser Ser Ser Asp Lys Pro		
	165	170

&lt;210&gt; 13

&lt;211&gt; 258

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 13

Met Ser Val Glu Asp Thr Gln Pro Leu Ile Thr His Leu Ile Glu Leu		
1	5	10
Arg Lys Arg Leu Leu Asn Cys Ile Ile Ser Val Ile Val Ile Phe Leu		
	20	25
Cys Leu Val Tyr Phe Ala Asn Asp Ile Tyr His Leu Val Ser Ala Pro		
	35	40
Leu Ile Lys Gln Leu Pro Gln Gly Ser Thr Met Ile Ala Thr Asp Val		
	50	55
Ala Ser Pro Phe Phe Thr Pro Ile Lys Leu Thr Phe Met Val Ser Leu		
	65	70
Ile Leu Ser Ala Pro Val Ile Leu Tyr Gln Val Trp Ala Phe Ile Ala		
	85	90

Pro Ala Leu Tyr Lys His Glu Arg Arg Leu Val Val Pro Leu Leu Val  
 100 105 110

Ser Ser Ser Leu Leu Phe Tyr Ile Gly Met Ala Phe Ala Tyr Phe Val  
 115 120 125

Val Phe Pro Leu Ala Phe Gly Phe Leu Ala Asn Thr Ala Pro Glu Gly  
 130 135 140

Val Gln Val Ser Thr Asp Ile Ala Ser Tyr Leu Ser Phe Val Met Ala  
 145 150 155 160

Leu Phe Met Ala Phe Gly Val Ser Phe Glu Val Pro Val Ala Ile Val  
 165 170 175

Leu Leu Cys Trp Met Gly Ile Thr Ser Pro Glu Asp Leu Arg Lys Lys  
 180 185 190

Arg Pro Tyr Val Leu Val Gly Ala Phe Val Val Gly Met Leu Leu Thr  
 195 200 205

Pro Pro Asp Val Phe Ser Gln Thr Leu Leu Ala Ile Pro Met Tyr Cys  
 210 215 220

Leu Phe Glu Ile Gly Val Phe Phe Ser Arg Phe Tyr Val Gly Lys Gly  
 225 230 235 240

Arg Asn Arg Glu Glu Glu Asn Asp Ala Glu Ala Glu Ser Glu Lys Thr  
 245 250 255

Glu Glu

<210> 14

<211> 264

<212> PRT

<213> Escherichia coli

<400> 14

Met Glu Tyr Arg Met Phe Asp Ile Gly Val Asn Leu Thr Ser Ser Gln  
 1 5 10 15

Phe Ala Lys Asp Arg Asp Asp Val Val Ala Arg Ala Phe Asp Ala Gly  
 20 25 30

Val Asn Gly Leu Leu Ile Thr Gly Thr Asn Leu Arg Glu Ser Gln Gln  
 35 40 45

Ala Gln Lys Leu Ala Arg Gln Tyr Ser Ser Cys Trp Ser Thr Ala Gly  
 50 55 60

Val	His	Pro	His	Asp	Ser	Ser	Gln	Trp	Gln	Ala	Val	Thr	Glu	Glu	Ala	65	70	75	80
Ile	Ile	Glu	Leu	Ala	Ala	Gln	Pro	Glu	Val	Val	Ala	Ile	Gly	Glu	Cys	85	90	95	
Gly	Leu	Asp	Phe	Asn	Arg	Asn	Phe	Ser	Thr	Pro	Glu	Glu	Gln	Glu	Arg	100	105	110	
Ala	Phe	Val	Ala	Gln	Leu	Arg	Ile	Ala	Ala	Glu	Leu	Asn	Met	Pro	Val	115	120	125	
Phe	Met	His	Cys	Arg	Asp	Ala	His	Glu	Arg	Phe	Met	Thr	Leu	Leu	Glu	130	135	140	
Pro	Trp	Leu	Asp	Lys	Leu	Pro	Gly	Ala	Val	Leu	His	Cys	Phe	Thr	Gly	145	150	155	160
Thr	Arg	Glu	Glu	Met	Gln	Ala	Cys	Val	Ala	Cys	Gly	Ile	Tyr	Ile	Gly	165	170	175	
Ile	Thr	Gly	Trp	Val	Cys	Asp	Glu	Arg	Arg	Gly	Leu	Glu	Leu	Arg	Glu	180	185	190	
Leu	Leu	Pro	Leu	Ile	Pro	Ala	Glu	Lys	Leu	Leu	Ile	Glu	Thr	Asp	Ala	195	200	205	
Pro	Tyr	Leu	Leu	Pro	Arg	Asp	Leu	Thr	Pro	Lys	Pro	Ser	Ser	Arg	Arg	210	215	220	
Asn	Glu	Pro	Ala	His	Leu	Pro	His	Ile	Leu	Gln	Arg	Ile	Ala	His	Trp	225	230	235	240
Arg	Gly	Glu	Asp	Ala	Ala	Trp	Leu	Ala	Ala	Thr	Thr	Asp	Ala	Asn	Val	245	250	255	
Lys	Thr	Leu	Phe	Gly	Ile	Ala	Phe									260			

&lt;210&gt; 15

&lt;211&gt; 586

&lt;212&gt; DNA

&lt;213&gt; Escherichia coli

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (170)..(370)

&lt;400&gt; 15



tcttaaaca cgcgcgttt gcgccgccgc aattattatg atgttttttt actcggcgct 60  
 tgattcacct tgttacagat tgctattgtg tgcgcgcgtc gaatgaccgt taatattctc 120  
 tggtttttaa ggcgcgttct gttgccggtt atatgtcaag aaggatatct atg ggt gag 178  
 Met Gly Glu  
 1

att agt att acc aaa ctg ctg gta gtt gcg gcg ctg gtc gtt ctg ctg 226  
 Ile Ser Ile Thr Lys Leu Leu Val Val Ala Ala Leu Val Val Leu Leu  
 5 10 15

ttt ggg act aag aag tta cgt acg ctg ggc gga gac ctt gga gcg gcc 274  
 Phe Gly Thr Lys Lys Leu Arg Thr Leu Gly Gly Asp Leu Gly Ala Ala  
 20 25 30 35

att aaa ggg ttc aag aag gcg atg aat gat gac gat gct gcg gcg aaa 322  
 Ile Lys Gly Phe Lys Lys Ala Met Asn Asp Asp Asp Ala Ala Ala Lys  
 40 45 50

aaa ggc gca gac gtt gat ctt cag gct gaa aag ctc tct cat aaa gag 370  
 Lys Gly Ala Asp Val Asp Leu Gln Ala Glu Lys Leu Ser His Lys Glu  
 55 60 65

tgacgtggcg agcaggacgc tccctcaata tcttgttcga tacaaaaacc cgcttcaaaa 430

agcggggttt ttatcagaca gatgtaagta attattacag gattacttaa cttccatccc 490

tttcgcctgc aaatcggcgt ggtaagaaga gcggacaaac ggaccgcatg cagcatgggt 550

aaagcccatc gccagcgctt cgctttcatt tcgtcg 586

<210> 16

<211> 67

<212> PRT

<213> Escherichia coli

<400> 16

Met Gly Glu Ile Ser Ile Thr Lys Leu Leu Val Val Ala Ala Leu Val  
 1 5 10 15

Val Leu Leu Phe Gly Thr Lys Lys Leu Arg Thr Leu Gly Gly Asp Leu  
 20 25 30

Gly Ala Ala Ile Lys Gly Phe Lys Lys Ala Met Asn Asp Asp Asp Ala  
 35 40 45

Ala Ala Lys Lys Gly Ala Asp Val Asp Leu Gln Ala Glu Lys Leu Ser  
 50 55 60

His Lys Glu  
65

<210> 17  
<211> 4200  
<212> DNA  
<213> *Salmonella typhimurium*

<220>  
<221> CDS  
<222> (947) .. (1444)

<220>  
<221> CDS  
<222> (1450) .. (1722)

<400> 17  
cgcaagtcaa tgcgtccccg gtcgtatgta aaagtatgtg aatagggcgg gcgaaagcgg 60  
ctaacaaaga ggcagcgtga aggataatgt gtataatgcg gccctaataa ttcacatcatct 120  
atcacagagg aacatgtatg ggtggatatca gtatttggca gttgttgatt gttgccgtta 180  
tcgtcgtact gctgttcggc accaaaaaac tcggttccat cggttccgat cttggcgcgt 240  
ctatcaaagg ctttaaaaaag gccatgagcg atgatgatgc caaacaggat aaaaccagtc 300  
aggacgctga ttttaccgct aaatctatcg cggataagca aggcgaagcg aaaaaggaag 360  
acgctaaaag ccaagataaa gagcaggat aatccgtgtt tgatatcggg tttagcgaac 420  
tgctgttagt gttcgttatc ggcctcattg tgttggggcc gcaacgattg ccagtagcgg 480  
taaaaacggt agcgggctgg attcgcgcgt tgcggtccct tgcgacaacg gttcagaatg 540  
aactgactca ggaactgaaa cttcaggagt tccaggacag tctgaaaaaa gtcgaaaagg 600  
cgagcctgga aaatctgact cccgaactga aagcatctat ggatgaactg cgtcaggcgg 660  
cggagtcgat gaaacgcacc tacagcgcta acgatcccga acaagcgagc gatgaagcgc 720  
ataccatcca taatccggtg gtaaaaggga acgaaacgca gcatgagggc gtcacccctg 780  
ccgccgctga aacacaggcg agcgcgccgg aacaaaagcc ggagcccgtt aaagctaacg 840  
tgcttgagtc gacggaaacc gtttccgtag ccacgataga cgccgagaag aaatccgctg 900  
cgctgttgt cgaatcttcc ccctcgtcga gtgataaacc gtaaac atg gct gta 955  
Met Ala Val

1

gaa gat act caa ccg ctt atc acg cat ctg atc gag ttg cgt aag cgc	1003
Glu Asp Thr Gln Pro Leu Ile Thr His Leu Ile Glu Leu Arg Lys Arg	
5 10 15	
ctg cta aac tgc atc gtc gca gta ctt ctg att ttt ctg gcg tta att	1051
Leu Leu Asn Cys Ile Val Ala Val Leu Leu Ile Phe Leu Ala Leu Ile	
20 25 30 35	
tat ttc gcc aat gat att tat cat tta gtc gcc gca ccg ctg att aaa	1099
Tyr Phe Ala Asn Asp Ile Tyr His Leu Val Ala Ala Pro Leu Ile Lys	
40 45 50	
cag atg ccg caa ggg gcg aca atg att gcg acg gat gtg gcg tcg ccg	1147
Gln Met Pro Gln Gly Ala Thr Met Ile Ala Thr Asp Val Ala Ser Pro	
55 60 65	
ttt ttt acg cct atc aaa ctc acc ttc atg gtg tct ttg atc tta tcc	1195
Phe Phe Thr Pro Ile Lys Leu Thr Phe Met Val Ser Leu Ile Leu Ser	
70 75 80	
gcg cct gtc att ttg tac cag gtt tgg gcc ttt atc gcc ccg gcg ctg	1243
Ala Pro Val Ile Leu Tyr Gln Val Trp Ala Phe Ile Ala Pro Ala Leu	
85 90 95	
tat aag cat gag cgt cgt ctg gtc gta cct ctg ctg gta tcc agc tcg	1291
Tyr Lys His Glu Arg Arg Leu Val Val Pro Leu Leu Val Ser Ser Ser	
100 105 110 115	
ctg ctt ttc tat att ggt atg gcc ttc gcc tat ttt gtc gta ttc cct	1339
Leu Leu Phe Tyr Ile Gly Met Ala Phe Ala Tyr Phe Val Val Phe Pro	
120 125 130	
ttg gcc ttt ggt ttc ctg acg cat acg gcg ccg gaa ggg gta cag gtt	1387
Leu Ala Phe Gly Phe Leu Thr His Thr Ala Pro Glu Gly Val Gln Val	
135 140 145	
tcg aca gat atc gcc agc tat ctt agc ttt gtc atg gcg ctt ttt atg	1435
Ser Thr Asp Ile Ala Ser Tyr Leu Ser Phe Val Met Ala Leu Phe Met	
150 155 160	
gcc ttt gcg tagcc ttt gaa gtg ccg gtg gcg att gtg ttg ctg tgc tgg	1485
Ala Phe Ala Phe Glu Val Pro Val Ala Ile Val Leu Leu Cys Trp	
165 170 175	
atg ggc atc acc acg cca gaa gat ttg cgt aaa aaa cgg cct tat atc	1533
Met Gly Ile Thr Thr Pro Glu Asp Leu Arg Lys Lys Arg Pro Tyr Ile	
180 185 190	
ctg gtc ggg gca ttc att gtg gga atg ctg ctt acg ccg cca gat gtt	1581

G:\SH-APPS\Seq\gje-65.txt\DNB\srp

aagcgcacaa aatggctgac gccgcgcgtg gcgttgattg tagtggtatg tatcacttcc 2862  
ggatcaaatt caacgaacag ataattagga aagagcgggt cgctgacgga ggtacgtttt 2922  
ccgcgtacca ttttttccag ggtgatcatc ggtgtcaggc aacttaccgc ttgtctttcg 2982  
aggtgttcct gagcacgctg aagttgcccg cgtttgacgt acagtaaata ccaggattgc 3042  
ataatgactc ttatccgctt gttcggggcg caagcatagc aaaagccatg cgcgaaagta 3102  
attatacact tcatccttta agccgtatct ggattagcgt tggttgccag agttcacgct 3162  
aatttaacaa aaatacagca tcccgatgat gaacgccgta taatgatgcg cttaccaaga 3222  
ggctacaatg gacgccatga aatatcacga tttacgcgac ttcctgacgc tacttgagca 3282  
gcagggggaa ctaaaacgca tcacgctacc tgtggatcct catctggaaa tcacggaaat 3342  
cgctgaccgc acgctgcgtg ccggtggacc ggcgttgctg tttgaaaatc ctaaaggta 3402  
cgccatgccg gtgctgtgca accttttttg cacgcaaaa cgctggcgga tgggcatggg 3462  
gcaggatgat gtttccgcct tacgggaagt gggtaaatta ttagcgtttc ttaaagaacc 3522  
tgagccgccg aaagcgtttc gcgatctgtt tgacaagctg ccgcagtta agcaagtgc 3582  
gaatatgccg acgaaacggt tacgcggcgc gccttgccag cagaaaatcg cgtctggcga 3642  
tgatgtcgat ttaacgcgtc ttcctgtcat gacctgttg ccggacgac ccgcgccgct 3702  
gattacctgg ggactgacgg taacgcgtgg tccgcacaaa gagcggcaaa acctgggcat 3762  
ttatcgtcag cagttgatag gtaaaaaataa gctgattatg cgctggctgt ctcaccgcgg 3822  
cggcgcgctg gatthtcagg agtggttagc cgcgctccg ggtgaacgtt tcccggtctc 3882  
cgtcgattg ggcgccgatc cggcacgata cttggcgccg tgactcctgt tcccgatact 3942  
ctgtcggagt atgcctttgc gggcctgctg cgcggcacga aaactgaagt ggttaatgct 4002  
ttctacgatc tggagtgcgt cagcgcgaga tatcttgaag tacatgagcg gagagatgcg 4062  
cggagacgta tgcgatcata cggcatatat gaggatagc tcgtcttacg tcacgcaata 4122  
acagcgtaga tgcattata tcactatacg cgcgcatgag ctcgtatagg tgcctcatat 4182  
ctcgtctatc tcaaagtc 4200

<210> 18

<211> 166

&lt;212&gt; PRT

&lt;213&gt; Salmonella typhimurium

&lt;400&gt; 18

Met Ala Val Glu Asp Thr Gln Pro Leu Ile Thr His Leu Ile Glu Leu  
 1 5 10 15

Arg Lys Arg Leu Leu Asn Cys Ile Val Ala Val Leu Leu Ile Phe Leu  
 20 25 30

Ala Leu Ile Tyr Phe Ala Asn Asp Ile Tyr His Leu Val Ala Ala Pro  
 35 40 45

Leu Ile Lys Gln Met Pro Gln Gly Ala Thr Met Ile Ala Thr Asp Val  
 50 55 60

Ala Ser Pro Phe Phe Thr Pro Ile Lys Leu Thr Phe Met Val Ser Leu  
 65 70 75 80

Ile Leu Ser Ala Pro Val Ile Leu Tyr Gln Val Trp Ala Phe Ile Ala  
 85 90 95

Pro Ala Leu Tyr Lys His Glu Arg Arg Leu Val Val Pro Leu Leu Val  
 100 105 110

Ser Ser Ser Leu Leu Phe Tyr Ile Gly Met Ala Phe Ala Tyr Phe Val  
 115 120 125

Val Phe Pro Leu Ala Phe Gly Phe Leu Thr His Thr Ala Pro Glu Gly  
 130 135 140

Val Gln Val Ser Thr Asp Ile Ala Ser Tyr Leu Ser Phe Val Met Ala  
 145 150 155 160

Leu Phe Met Ala Phe Ala  
 165

&lt;210&gt; 19

&lt;211&gt; 91

&lt;212&gt; PRT

&lt;213&gt; Salmonella typhimurium

&lt;400&gt; 19

Phe Glu Val Pro Val Ala Ile Val Leu Leu Cys Trp Met Gly Ile Thr  
 1 5 10 15

Thr Pro Glu Asp Leu Arg Lys Lys Arg Pro Tyr Ile Leu Val Gly Ala  
 20 25 30

Phe Ile Val Gly Met Leu Leu Thr Pro Pro Asp Val Phe Ser Gln Thr

35	40	45
Leu Leu Ala Ile Pro Met Tyr Cys Leu Phe Glu Ile Gly Val Phe Cys		
50	55	60
Ser Arg Phe Tyr Val Gly Lys Arg Arg Thr Arg Asp Glu Asp Asn Glu		
65	70	75
Ala Glu Thr Glu Lys Ala Glu His Thr Glu Asp		
85	90	

<210> 20  
 <211> 2601  
 <212> DNA  
 <213> *Neisseria meningitidis*

<220>  
 <221> CDS  
 <222> (1572)..(2339)

<400> 20  
 agacaaaatc ctaaaaaaag tgattgaaga ggcgggcgaa gtgttgatgg catccaaaga 60  
 caaaaacccg tcccacctgg tttacgaagt tgccgactta tggtttcaca ccatgattct 120  
 tctgacacac cacgacctga aggcggaaga cgtattggac gaacttgccg gccgccaagg 180  
 tttgtcgggc ttggccgaaa aagccgctcg cacagaatct tgaatttata ttaaaatccg 240  
 cactttccca cattcaatcc gtctgaccgc tgttcagacg gcatcggagc cgttatggac 300  
 aactgtatatt tctgcaaaat cgccgcaaaa gacattccgg cgcaaaccgt ctatgaagac 360  
 ggcgaaatgg tttgtttcaa agacatcaac cccgctgctc cggttcatct gctgctgatt 420  
 cccaaagtcc atttcgattc gttggcacac gccgcgccc aacatcagcc ctttttggga 480  
 aaaatgatgc tgaaagtcc cgaaatcgcc aaagcggcag gactggcaga cggcttcaaa 540  
 accctgatca acaccggaag aggcggcgga caagaggtct tccacctgca tatacacatc 600  
 atgggcacac ccgtataaac cgttatttca caatcaaccc ctaatactta ctttaaggata 660  
 catcatgggc agttttttctc tgacgcactg gattatcgta ctgattatcg tcgttttgat 720  
 attcggcacc aaaaaactgc gcaacgtcgg caaagacctc ggcggtgcgg ttcattgactt 780  
 caaacagggg ctgaacgaag gtacagacgg caaagaagcc caaaaagacg atgtaatcga 840

```

acacaaaaaa gacgaagaca aagcgtaatt tatgtttgat ttcggtttgg gcgagctggt 900
ttttgtcggc attatcgccc tgattgtcct cggccccgaa cgcctgcccg aggccgcccg 960
caccgcccga cggctcatcg gcaggctgca acgctttgtc ggcagcgtca aacaggaatt 1020
tgacacgcaa atcgaactgg aagaactaag gaaggcaaag caggaatttg aagctgcccgc 1080
tgctcagggt cgagacagcc tcaaagaaac cggtagcgat atggagggtg atctgcacga 1140
catttccgac ggtctgaagc cttgggaaaa actgccccgaa cagcgcacgc ctgctgattt 1200
cgggtgtcgat gaaaacggca atccctttcc cgatgcggca aacaccctat tagacggcat 1260
ttccgacgtt atgccgtccg aacgttccta cgcttccgcc gaaacccttg gggacagcgg 1320
gcaaaccggc agtacagccg aaccgcgga aaccgaccaa gaccgtgcat ggcgggaata 1380
cctgactgct tctgccgccg caccgctcgt acagaccgtc gaagtcagct atatcgatac 1440
cgctgttgaa acccctgttc cgcataccac ttcgctgcgt aaacaggcaa taagccgcaa 1500
acgcgatttg cgtcctaaat cccgcgccaa acctaaattg cgcgtccgta aatcataaag 1560
agggcaatcc g gtg tcc gaa aca caa aac gaa caa ccc gtc caa ccg ctt 1610
                Val Ser Glu Thr Gln Asn Glu Gln Pro Val Gln Pro Leu
                  1             5             10

gtc gag cat ctc atc gag ctg cgc cgc cgc ctg atg tgg acg gtt gtc 1658
Val Glu His Leu Ile Glu Leu Arg Arg Arg Leu Met Trp Thr Val Val
    15             20             25

ggg atc tta gtc tgc ttt ttc ggc cta atg ccg ttt gcc caa caa ctc 1706
Gly Ile Leu Val Cys Phe Phe Gly Leu Met Pro Phe Ala Gln Gln Leu
    30             35             40             45

tat act ttt atc gcc gac ccg ctg atg gca aac ctg ccc aaa gac acc 1754
Tyr Thr Phe Ile Ala Asp Pro Leu Met Ala Asn Leu Pro Lys Asp Thr
    50             55             60

agc atg att gcc acc gat gtc atc gca cca ttt ttc gtg ccg gtc aaa 1802
Ser Met Ile Ala Thr Asp Val Ile Ala Pro Phe Phe Val Pro Val Lys
    65             70             75

gtt acc ctg atg gcg gca ttt tta att tcg ctg ccg cat acg ctc tac 1850
Val Thr Leu Met Ala Ala Phe Leu Ile Ser Leu Pro His Thr Leu Tyr
    80             85             90

caa atc tgg gca ttc gtc gcc ccc gca ctc tac caa aac gaa aaa cgc 1898
Gln Ile Trp Ala Phe Val Ala Pro Ala Leu Tyr Gln Asn Glu Lys Arg
    95             100            105

```



```

ctg att acg ccg ctc gtc ctc tcc agc gtc agc ctg ttt ttc atc ggc 1946
Leu Ile Thr Pro Leu Val Leu Ser Ser Val Ser Leu Phe Phe Ile Gly
110                115                120                125

atg gca ttt gcc tac ttt ttg gtt ttc ccc gtc att ttc aaa ttc ctt 1994
Met Ala Phe Ala Tyr Phe Leu Val Phe Pro Val Ile Phe Lys Phe Leu
                130                135                140

gcc agc gtt acc cct gtc ggt gtc aat atg gcg aca gac atc gac aaa 2042
Ala Ser Val Thr Pro Val Gly Val Asn Met Ala Thr Asp Ile Asp Lys
                145                150                155

tac ctc tcc ttc atc ttg ggg atg ttt gtc gca ttc ggt aca acg ttt 2090
Tyr Leu Ser Phe Ile Leu Gly Met Phe Val Ala Phe Gly Thr Thr Phe
                160                165                170

gaa gtc ccc att gtc gtt atc ctg tta acc aaa att ggt gtg gta aca 2138
Glu Val Pro Ile Val Val Ile Leu Leu Thr Lys Ile Gly Val Val Thr
                175                180                185

acc gaa cag ctc aaa cgc gcc cgc ccc tat gtg att gtc ggc gcg ttt 2186
Thr Glu Gln Leu Lys Arg Ala Arg Pro Tyr Val Ile Val Gly Ala Phe
190                195                200                205

gtc att gcc gcc atc atc acg ccg ccc gat gtg att tca caa acc ctg 2234
Val Ile Ala Ala Ile Ile Thr Pro Pro Asp Val Ile Ser Gln Thr Leu
                210                215                220

ctt gcc att ccg ctg att ctc tta tac gaa gca ggt att tgg ttc gga 2282
Leu Ala Ile Pro Leu Ile Leu Leu Tyr Glu Ala Gly Ile Trp Phe Gly
                225                230                235

cgc ttt ttc acg cca cgt tca gaa cag gat ggc gac ata cag ccg cct 2330
Arg Phe Phe Thr Pro Arg Ser Glu Gln Asp Gly Asp Ile Gln Pro Pro
                240                245                250

gca aca acc tgacactatg ccgtccgaac ctccgcctca taccgccaca 2379
Ala Thr Thr
255

gattaaggaa tacctttgaa taccctctat ttaggttcaa acagcccgcg ccgaatggaa 2439

atcctgacac agttgggcta tcaggctcgtc aagctgcctg ccaacatcga cgaaacggtc 2499

agacagaacg aagaccctgc ccgttacgtt caaaggatgg cagaagaaaa aaaccgaacc 2559

gccctgaccc tctttttgcga aaccaacggc acaatgcccc at 2601

```

&lt;210&gt; 21

&lt;211&gt; 256

&lt;212&gt; PRT

&lt;213&gt; Neisseria meningitidis

&lt;400&gt; 21

Val	Ser	Glu	Thr	Gln	Asn	Glu	Gln	Pro	Val	Gln	Pro	Leu	Val	Glu	His
1				5				10						15	
Leu	Ile	Glu	Leu	Arg	Arg	Arg	Leu	Met	Trp	Thr	Val	Val	Gly	Ile	Leu
			20				25						30		
Val	Cys	Phe	Phe	Gly	Leu	Met	Pro	Phe	Ala	Gln	Gln	Leu	Tyr	Thr	Phe
		35					40					45			
Ile	Ala	Asp	Pro	Leu	Met	Ala	Asn	Leu	Pro	Lys	Asp	Thr	Ser	Met	Ile
	50					55					60				
Ala	Thr	Asp	Val	Ile	Ala	Pro	Phe	Phe	Val	Pro	Val	Lys	Val	Thr	Leu
65					70					75					80
Met	Ala	Ala	Phe	Leu	Ile	Ser	Leu	Pro	His	Thr	Leu	Tyr	Gln	Ile	Trp
				85					90					95	
Ala	Phe	Val	Ala	Pro	Ala	Leu	Tyr	Gln	Asn	Glu	Lys	Arg	Leu	Ile	Thr
			100					105					110		
Pro	Leu	Val	Leu	Ser	Ser	Val	Ser	Leu	Phe	Phe	Ile	Gly	Met	Ala	Phe
		115					120					125			
Ala	Tyr	Phe	Leu	Val	Phe	Pro	Val	Ile	Phe	Lys	Phe	Leu	Ala	Ser	Val
	130					135					140				
Thr	Pro	Val	Gly	Val	Asn	Met	Ala	Thr	Asp	Ile	Asp	Lys	Tyr	Leu	Ser
145					150					155				160	
Phe	Ile	Leu	Gly	Met	Phe	Val	Ala	Phe	Gly	Thr	Thr	Phe	Glu	Val	Pro
			165						170				175		
Ile	Val	Val	Ile	Leu	Leu	Thr	Lys	Ile	Gly	Val	Val	Thr	Thr	Glu	Gln
			180					185					190		
Leu	Lys	Arg	Ala	Arg	Pro	Tyr	Val	Ile	Val	Gly	Ala	Phe	Val	Ile	Ala
		195					200					205			
Ala	Ile	Ile	Thr	Pro	Pro	Asp	Val	Ile	Ser	Gln	Thr	Leu	Leu	Ala	Ile
	210					215					220				
Pro	Leu	Ile	Leu	Leu	Tyr	Glu	Ala	Gly	Ile	Trp	Phe	Gly	Arg	Phe	Phe
225					230					235				240	
Thr	Pro	Arg	Ser	Glu	Gln	Asp	Gly	Asp	Ile	Gln	Pro	Pro	Ala	Thr	Thr
			245						250					255	

<210> 22  
 <211> 4604  
 <212> DNA  
 <213> Escherichia coli

<220>  
 <221> CDS  
 <222> (2982)..(4082)

<220>  
 <221> CDS  
 <222> (1534)..(2637)

<220>  
 <221> CDS  
 <222> (749)..(1531)

<220>  
 <221> CDS  
 <222> (6)..(746)

<400> 22  
 ggcta gtt gat gat aat ttg aaa ggt caa ggt gca gga aaa aat ttt tta 50  
 Val Asp Asp Asn Leu Lys Gly Gln Gly Ala Gly Lys Asn Phe Leu  
 1 5 10 15

tcg ctg ata aag tac agc gag aca gat tat aca att tat tgt gac caa 98  
 Ser Leu Ile Lys Tyr Ser Glu Thr Asp Tyr Thr Ile Tyr Cys Asp Gln  
 20 25 30

gat gat att tgg tta gaa aac aaa ata ttt gaa tta gta aag tat gca 146  
 Asp Asp Ile Trp Leu Glu Asn Lys Ile Phe Glu Leu Val Lys Tyr Ala  
 35 40 45

aat gaa att aaa ttg aat gta tca gat gcg cct tcg cta gtt tat gct 194  
 Asn Glu Ile Lys Leu Asn Val Ser Asp Ala Pro Ser Leu Val Tyr Ala  
 50 55 60

gat ggc tat gct tat atg gat ggt gag ggt aca atc gat ttt tct ggg 242  
 Asp Gly Tyr Ala Tyr Met Asp Gly Glu Gly Thr Ile Asp Phe Ser Gly  
 65 70 75

ata tct aac aat cat gct gat caa tta aag gat ttt ctt ttt ttt aat 290  
 Ile Ser Asn Asn His Ala Asp Gln Leu Lys Asp Phe Leu Phe Phe Asn  
 80 85 90 95

ggg gga tac caa gga tgt tct att atg ttc aat cgt gca atg acc aaa 338  
 Gly Gly Tyr Gln Gly Cys Ser Ile Met Phe Asn Arg Ala Met Thr Lys  
 100 105 110

ttt ctt ctg aat tat cga gga ttt gta tat cta cat gac gat atc aca	386
Phe Leu Leu Asn Tyr Arg Gly Phe Val Tyr Leu His Asp Asp Ile Thr	
115 120 125	
aca tta gct gca tac gct ctt ggt aaa gtt tat ttt ctc ccg aaa tac	434
Thr Leu Ala Ala Tyr Ala Leu Gly Lys Val Tyr Phe Leu Pro Lys Tyr	
130 135 140	
ctt atg tta tat aga cag cac acg aat gcg gta act ggt atc aaa aca	482
Leu Met Leu Tyr Arg Gln His Thr Asn Ala Val Thr Gly Ile Lys Thr	
145 150 155	
ttc cgc aat gga ttg act tct aaa ttt aaa tca cca gta aac tat ctt	530
Phe Arg Asn Gly Leu Thr Ser Lys Phe Lys Ser Pro Val Asn Tyr Leu	
160 165 170 175	
tta tca cga aaa cat tat cag gta aaa aaa tct ttt ttt gaa tgt aac	578
Leu Ser Arg Lys His Tyr Gln Val Lys Lys Ser Phe Phe Glu Cys Asn	
180 185 190	
agc tct atc tta tca gag acg aat aaa aaa gtt ttt ttg gat ttt att	626
Ser Ser Ile Leu Ser Glu Thr Asn Lys Lys Val Phe Leu Asp Phe Ile	
195 200 205	
tca ttt tgt gaa tca aat aat aaa ttt aca gat ttt ttt aag tta tgg	674
Ser Phe Cys Glu Ser Asn Asn Lys Phe Thr Asp Phe Phe Lys Leu Trp	
210 215 220	
cga ggt ggg ttt aga tta aat aac agt aga act aaa tta tta tta aaa	722
Arg Gly Gly Phe Arg Leu Asn Asn Ser Arg Thr Lys Leu Leu Leu Lys	
225 230 235	
ttc tta ata cgg aga aaa ttt agc ga atg att tca ata ctt aca cct	769
Phe Leu Ile Arg Arg Lys Phe Ser Met Ile Ser Ile Leu Thr Pro	
240 245 250	
act ttt aat cgg caa cat act tta tca agg cta ttc aat tct ctt ata	817
Thr Phe Asn Arg Gln His Thr Leu Ser Arg Leu Phe Asn Ser Leu Ile	
255 260 265 270	
tta caa act gat aaa gat ttt gag tgg ata ata att gat gat ggt agt	865
Leu Gln Thr Asp Lys Asp Phe Glu Trp Ile Ile Ile Asp Asp Gly Ser	
275 280 285	
ata gat gca aca gcg gta ctt gta gaa gat ttt aga aaa aaa tgt gat	913
Ile Asp Ala Thr Ala Val Leu Val Glu Asp Phe Arg Lys Lys Cys Asp	
290 295 300	
ttt gac ttg att tat tgc tat cag gaa aat aat ggt aag ccc atg gct	961
Phe Asp Leu Ile Tyr Cys Tyr Gln Glu Asn Asn Gly Lys Pro Met Ala	
305 310 315	

tta aac gct ggt gtt aaa gct tgt aga ggc gat tat atc ttt att gtt	1009
Leu Asn Ala Gly Val Lys Ala Cys Arg Gly Asp Tyr Ile Phe Ile Val	
320 325 330	
gac agt gat gat gca cta act ccc gat gcc ata aaa tta att aaa gaa	1057
Asp Ser Asp Asp Ala Leu Thr Pro Asp Ala Ile Lys Leu Ile Lys Glu	
335 340 345 350	
tca ata cat gat tgc tta tct gag aag gaa agt ttc agc gga gtc ggt	1105
Ser Ile His Asp Cys Leu Ser Glu Lys Glu Ser Phe Ser Gly Val Gly	
355 360 365	
ttt aga aaa gca tat ata aaa ggg ggg att att ggt aat gat tta aat	1153
Phe Arg Lys Ala Tyr Ile Lys Gly Gly Ile Ile Gly Asn Asp Leu Asn	
370 375 380	
aat tct tca gaa cat ata tac tat tta aat gcg act gag att agc aat	1201
Asn Ser Ser Glu His Ile Tyr Tyr Leu Asn Ala Thr Glu Ile Ser Asn	
385 390 395	
tta ata aat ggt gat gtt gca tat tgt ttt aaa aaa gaa agt ttg gta	1249
Leu Ile Asn Gly Asp Val Ala Tyr Cys Phe Lys Lys Glu Ser Leu Val	
400 405 410	
aaa aat cca ttc ccc cgt ata gaa gat gaa aaa ttt gtt cca gaa tta	1297
Lys Asn Pro Phe Pro Arg Ile Glu Asp Glu Lys Phe Val Pro Glu Leu	
415 420 425 430	
tat att tgg aat aaa ata act gac aag gcg aag att cga ttt aac ata	1345
Tyr Ile Trp Asn Lys Ile Thr Asp Lys Ala Lys Ile Arg Phe Asn Ile	
435 440 445	
agc aaa gtt ata tat ctt tgt gag tat ctt gat gat ggt ctt tct aaa	1393
Ser Lys Val Ile Tyr Leu Cys Glu Tyr Leu Asp Asp Gly Leu Ser Lys	
450 455 460	
aat ttc cat aac cag ctt aaa aaa tac cca aag ggg ttt aag att tat	1441
Asn Phe His Asn Gln Leu Lys Lys Tyr Pro Lys Gly Phe Lys Ile Tyr	
465 470 475	
tac aaa gat caa aga aaa cga gag aaa act tat ata aaa aaa aca aag	1489
Tyr Lys Asp Gln Arg Lys Arg Glu Lys Thr Tyr Ile Lys Lys Thr Lys	
480 485 490	
atg cta att aga tat ttg caa tgt tgt tat tat gag aaa ata aa atg	1536
Met Leu Ile Arg Tyr Leu Gln Cys Cys Tyr Tyr Glu Lys Ile Met	
495 500 505	
aaa ata cta ttt gtc att aca ggt tta ggc ctt gga ggt gct gag aag	1584
Lys Ile Leu Phe Val Ile Thr Gly Leu Gly Leu Gly Gly Ala Glu Lys	
510 515 520 525	

cag gtt tgt ctt tta gct gat aaa tta agt tta agc ggg cac cat gta	1632
Gln Val Cys Leu Leu Ala Asp Lys Leu Ser Leu Ser Gly His His Val	
530 535 540	
aag att att tca ctt gga cat atg tct aat aat aaa gtc ttt cct agc	1680
Lys Ile Ile Ser Leu Gly His Met Ser Asn Asn Lys Val Phe Pro Ser	
545 550 555	
gaa aat aat gtt aat gtc att aat gta aat atg tca aaa aac att tct	1728
Glu Asn Asn Val Asn Val Ile Asn Val Asn Met Ser Lys Asn Ile Ser	
560 565 570	
gga gtt ata aaa ggt tgt gtc aga att aga gat gtt ata gct aat ttc	1776
Gly Val Ile Lys Gly Cys Val Arg Ile Arg Asp Val Ile Ala Asn Phe	
575 580 585	
aaa cca gac att gta cac agt cat atg ttt cat gca aac att atc act	1824
Lys Pro Asp Ile Val His Ser His Met Phe His Ala Asn Ile Ile Thr	
590 595 600 605	
aga ttg tct gta att gga atc aaa aac aga cct ggt att ata tca act	1872
Arg Leu Ser Val Ile Gly Ile Lys Asn Arg Pro Gly Ile Ile Ser Thr	
610 615 620	
gca cat aat aaa aat gaa ggt ggg tat ttc aga atg ctc aca tat aga	1920
Ala His Asn Lys Asn Glu Gly Gly Tyr Phe Arg Met Leu Thr Tyr Arg	
625 630 635	
ata acc gat tgt tta agt gat tgt tgt aca aat gtt agc aaa gaa gca	1968
Ile Thr Asp Cys Leu Ser Asp Cys Cys Thr Asn Val Ser Lys Glu Ala	
640 645 650	
gtg gat gag ttt tta cgg ata aaa gcc ttt aat ccc gct aaa gca att	2016
Val Asp Glu Phe Leu Arg Ile Lys Ala Phe Asn Pro Ala Lys Ala Ile	
655 660 665	
act atg tat aat ggg ata gat acc aat aaa ttt aaa ttt gat tta ttg	2064
Thr Met Tyr Asn Gly Ile Asp Thr Asn Lys Phe Lys Phe Asp Leu Leu	
670 675 680 685	
gca agg agg gaa att cga gac ggt att aat ata aaa aat gat gat ata	2112
Ala Arg Arg Glu Ile Arg Asp Gly Ile Asn Ile Lys Asn Asp Asp Ile	
690 695 700	
tta tta ctt gct gca ggt cgt tta acg tta gct aaa gat tat cct aat	2160
Leu Leu Leu Ala Ala Gly Arg Leu Thr Leu Ala Lys Asp Tyr Pro Asn	
705 710 715	
tta ttg aat gca atg act ctg ctt cct gaa cac ttt aaa ctt att att	2208
Leu Leu Asn Ala Met Thr Leu Leu Pro Glu His Phe Lys Leu Ile Ile	
720 725 730	

```

att ggt gat ggt gaa ttg cgt gac gaa att aat atg ctt ata aaa aaa 2256
Ile Gly Asp Gly Glu Leu Arg Asp Glu Ile Asn Met Leu Ile Lys Lys
735 740 745

ttg caa tta tct aat agg gtg tcc ttg ttg gga gtt aaa aaa aat att 2304
Leu Gln Leu Ser Asn Arg Val Ser Leu Leu Gly Val Lys Lys Asn Ile
750 755 760 765

gct ccc tat ttt tct gca tgt gat att ttt gtt ctc tct tct cgt tgg 2352
Ala Pro Tyr Phe Ser Ala Cys Asp Ile Phe Val Leu Ser Ser Arg Trp
770 775 780

gaa gga ttt gga tta gtc gtg gca gaa gct atg tca tgt gag cga att 2400
Glu Gly Phe Gly Leu Val Val Ala Glu Ala Met Ser Cys Glu Arg Ile
785 790 795

gtt gtt ggc acg gat tca ggg gga gta aga gaa gtt att ggt gac gat 2448
Val Val Gly Thr Asp Ser Gly Gly Val Arg Glu Val Ile Gly Asp Asp
800 805 810

gat ttt ctt gta ccc ata tct gat tca aca caa ctt gca agc aaa att 2496
Asp Phe Leu Val Pro Ile Ser Asp Ser Thr Gln Leu Ala Ser Lys Ile
815 820 825

gaa aaa ttg tct ttg agc cag ata cgt gat cac att ggt ttt cgg aat 2544
Glu Lys Leu Ser Leu Ser Gln Ile Arg Asp His Ile Gly Phe Arg Asn
830 835 840 845

cgt gag cgt att tta aaa aat ttc tca ata gat act att att atg cag 2592
Arg Glu Arg Ile Leu Lys Asn Phe Ser Ile Asp Thr Ile Ile Met Gln
850 855 860

tgg caa gaa ctc tat gga act ata att tgc tca aaa cat gaa agg 2637
Trp Gln Glu Leu Tyr Gly Thr Ile Ile Cys Ser Lys His Glu Arg
865 870 875

tagatttata tttggaacgt gtcttttgtt tgaatttaat tcaatctcaa ttgagatttt 2697

tgtattttcaa aaataccatc atagctaacg atgattggta tttatttttaa gatgctttct 2757

ataaatatat tgacgtttttt aatgcgccga aacgattggg ctgggaacag agaagtaaaa 2817

ctgttttgag aatgaagagt ttttgagatg tttatggata ttaaaaattg atccagtga 2877

ttaattatatt ataataaatc aagatttaat gttaataaat gataatcttt tctgacactc 2937

atattaatta tgagtgggtac gtttggtaaa cggtaaacta ttat atg aca gct aga 2993
Met Thr Ala Arg
880

aca act aaa gtt ttg cac tta caa tta ctc cca ctc tta agt ggc gtt 3041

```

Thr Thr Lys Val Leu His Leu Gln Leu Leu Pro Leu Leu Ser Gly Val	
885 890 895	
caa agg gta aca tta aac gaa att agt gcg tta tat act gat tat gat	3089
Gln Arg Val Thr Leu Asn Glu Ile Ser Ala Leu Tyr Thr Asp Tyr Asp	
900 905 910	
tat aca cta gtt tgc tca aaa aaa ggt cca cta aca aaa gca ttg ctg	3137
Tyr Thr Leu Val Cys Ser Lys Lys Gly Pro Leu Thr Lys Ala Leu Leu	
915 920 925	
gaa tat gat gtc gat tgt cat tgt atc ccc gaa ctt acg aga gaa att	3185
Glu Tyr Asp Val Asp Cys His Cys Ile Pro Glu Leu Thr Arg Glu Ile	
930 935 940	
acc gta aag aat gat ttt aaa gca ttg ttc aag ctt tat aag ttc ata	3233
Thr Val Lys Asn Asp Phe Lys Ala Leu Phe Lys Leu Tyr Lys Phe Ile	
945 950 955 960	
aaa aaa gaa aaa ttt gac att gtg cat aca cat tct tca aaa aca ggt	3281
Lys Lys Glu Lys Phe Asp Ile Val His Thr His Ser Ser Lys Thr Gly	
965 970 975	
att ttg ggg cga gtt gct gcc aaa tta gca cgt gtt gga aag gtg atc	3329
Ile Leu Gly Arg Val Ala Ala Lys Leu Ala Arg Val Gly Lys Val Ile	
980 985 990	
cac act gta cat ggt ttt tct ttt cca gcc gca tct agt aaa aaa agt	3377
His Thr Val His Gly Phe Ser Phe Pro Ala Ala Ser Ser Lys Lys Ser	
995 1000 1005	
tat tac ctt tat ttt ttc atg gaa tgg ata gca aag ttc ttt acg gat	3425
Tyr Tyr Leu Tyr Phe Phe Met Glu Trp Ile Ala Lys Phe Phe Thr Asp	
1010 1015 1020	
aag tta atc gtc ttg aat gta gat gat gaa tat ata gca ata aac aaa	3473
Lys Leu Ile Val Leu Asn Val Asp Asp Glu Tyr Ile Ala Ile Asn Lys	
1025 1030 1035 1040	
tta aaa ttc aag cgg gat aaa gtt ttt tta att cct aat gga gta gac	3521
Leu Lys Phe Lys Arg Asp Lys Val Phe Leu Ile Pro Asn Gly Val Asp	
1045 1050 1055	
act gat aag ttt tct cct tta gaa aat aaa att tat agt agc acc ttg	3569
Thr Asp Lys Phe Ser Pro Leu Glu Asn Lys Ile Tyr Ser Ser Thr Leu	
1060 1065 1070	
aat cta gta atg gtt ggt aga tta tcc aag caa aaa gat cct gag aca	3617
Asn Leu Val Met Val Gly Arg Leu Ser Lys Gln Lys Asp Pro Glu Thr	
1075 1080 1085	



```

tta ttg ctt gct gtt gaa aaa ctg ctg aat gaa aat gtt aat gtt aag 3665
Leu Leu Leu Ala Val Glu Lys Leu Leu Asn Glu Asn Val Asn Val Lys
1090 1095 1100

ctg aca ctt gta gga gat ggt gaa cta aaa gaa cag tta gaa agc agg 3713
Leu Thr Leu Val Gly Asp Gly Glu Leu Lys Glu Gln Leu Glu Ser Arg
1105 1110 1115 1120

ttc aaa cgg caa gat gga cgt ata att ttt cat gga tgg tca gat aac 3761
Phe Lys Arg Gln Asp Gly Arg Ile Ile Phe His Gly Trp Ser Asp Asn
1125 1130 1135

att gtt aat att tta aaa gtt aat gat ctt ttt ata tta cct tct ctt 3809
Ile Val Asn Ile Leu Lys Val Asn Asp Leu Phe Ile Leu Pro Ser Leu
1140 1145 1150

tgg gag ggt atg cca tta gca att tta gaa gca ttg agc tgt gga ctt 3857
Trp Glu Gly Met Pro Leu Ala Ile Leu Glu Ala Leu Ser Cys Gly Leu
1155 1160 1165

cca tgt ata gtc act aat att cca ggt aat aat agc tta ata gaa gat 3905
Pro Cys Ile Val Thr Asn Ile Pro Gly Asn Asn Ser Leu Ile Glu Asp
1170 1175 1180

ggc tat aat ggt tgt ttg ttt gaa att aga gat tgt cag tta tta tct 3953
Gly Tyr Asn Gly Cys Leu Phe Glu Ile Arg Asp Cys Gln Leu Leu Ser
1185 1190 1195 1200

caa aaa atc atg tca tat gtt ggt aag cca gaa ctg att gca cag caa 4001
Gln Lys Ile Met Ser Tyr Val Gly Lys Pro Glu Leu Ile Ala Gln Gln
1205 1210 1215

tct acc aat gca cga tca ttt att ctg aaa aat tat gga tta gtt aaa 4049
Ser Thr Asn Ala Arg Ser Phe Ile Leu Lys Asn Tyr Gly Leu Val Lys
1220 1225 1230

aga aat aat aag gtc aga cag cta tat gat aat taaatgaaac cgaaaagtta 4102
Arg Asn Asn Lys Val Arg Gln Leu Tyr Asp Asn
1235 1240

aaaaagaaca gggttttcaa agtgaaaata aaattacagt ttttttattg caatgattaa 4162

cgtaacatct gcattacatt caagccgcac aaccccgcgg tgaccacccc tgacaggagt 4222

aaacaatgtc aaagcaacag atcggcgtcg tcggtatggc agtgatggga cgcaacctcg 4282

cgctcaacat cgaaagccgt gggtataccg tctctatttt caaccgttcc cgtgaaaaga 4342

cggaagaagt tattgccgaa aatccaggca agaaactggg tccttactat acggtgaaag 4402

agttcgttga atctcttgaa acgcctcgtc gcacccgtgtt aatgggttaa agcaggtgca 4462

```

ggcacggatg ctgctattga ttccctgaaa ccatatctcg ataaaggcga tatcatcatt 4522  
 gatgggtggg taataccttc tttcaggaca ccattcgtcg taaccgcgag ctttctgcac 4582  
 aaggctttac ttcacgcgta cc 4604

<210> 23  
 <211> 247  
 <212> PRT  
 <213> Escherichia coli

<400> 23  
 Val Asp Asp Asn Leu Lys Gly Gln Gly Ala Gly Lys Asn Phe Leu Ser  
   1                  5                  10                  15  
 Leu Ile Lys Tyr Ser Glu Thr Asp Tyr Thr Ile Tyr Cys Asp Gln Asp  
           20                  25                  30  
 Asp Ile Trp Leu Glu Asn Lys Ile Phe Glu Leu Val Lys Tyr Ala Asn  
           35                  40                  45  
 Glu Ile Lys Leu Asn Val Ser Asp Ala Pro Ser Leu Val Tyr Ala Asp  
           50                  55                  60  
 Gly Tyr Ala Tyr Met Asp Gly Glu Gly Thr Ile Asp Phe Ser Gly Ile  
           65                  70                  75                  80  
 Ser Asn Asn His Ala Asp Gln Leu Lys Asp Phe Leu Phe Phe Asn Gly  
                   85                  90                  95  
 Gly Tyr Gln Gly Cys Ser Ile Met Phe Asn Arg Ala Met Thr Lys Phe  
           100                  105                  110  
 Leu Leu Asn Tyr Arg Gly Phe Val Tyr Leu His Asp Asp Ile Thr Thr  
           115                  120                  125  
 Leu Ala Ala Tyr Ala Leu Gly Lys Val Tyr Phe Leu Pro Lys Tyr Leu  
           130                  135                  140  
 Met Leu Tyr Arg Gln His Thr Asn Ala Val Thr Gly Ile Lys Thr Phe  
           145                  150                  155                  160  
 Arg Asn Gly Leu Thr Ser Lys Phe Lys Ser Pro Val Asn Tyr Leu Leu  
           165                  170                  175  
 Ser Arg Lys His Tyr Gln Val Lys Lys Ser Phe Phe Glu Cys Asn Ser  
           180                  185                  190  
 Ser Ile Leu Ser Glu Thr Asn Lys Lys Val Phe Leu Asp Phe Ile Ser  
           195                  200                  205

Phe Cys Glu Ser Asn Asn Lys Phe Thr Asp Phe Phe Lys Leu Trp Arg  
 210 215 220

Gly Gly Phe Arg Leu Asn Asn Ser Arg Thr Lys Leu Leu Leu Lys Phe  
 225 230 235 240

Leu Ile Arg Arg Lys Phe Ser  
 245

<210> 24

<211> 261

<212> PRT

<213> Escherichia coli

<400> 24

Met Ile Ser Ile Leu Thr Pro Thr Phe Asn Arg Gln His Thr Leu Ser  
 1 5 10 15

Arg Leu Phe Asn Ser Leu Ile Leu Gln Thr Asp Lys Asp Phe Glu Trp  
 20 25 30

Ile Ile Ile Asp Asp Gly Ser Ile Asp Ala Thr Ala Val Leu Val Glu  
 35 40 45

Asp Phe Arg Lys Lys Cys Asp Phe Asp Leu Ile Tyr Cys Tyr Gln Glu  
 50 55 60

Asn Asn Gly Lys Pro Met Ala Leu Asn Ala Gly Val Lys Ala Cys Arg  
 65 70 75 80

Gly Asp Tyr Ile Phe Ile Val Asp Ser Asp Asp Ala Leu Thr Pro Asp  
 85 90 95

Ala Ile Lys Leu Ile Lys Glu Ser Ile His Asp Cys Leu Ser Glu Lys  
 100 105 110

Glu Ser Phe Ser Gly Val Gly Phe Arg Lys Ala Tyr Ile Lys Gly Gly  
 115 120 125

Ile Ile Gly Asn Asp Leu Asn Asn Ser Ser Glu His Ile Tyr Tyr Leu  
 130 135 140

Asn Ala Thr Glu Ile Ser Asn Leu Ile Asn Gly Asp Val Ala Tyr Cys  
 145 150 155 160

Phe Lys Lys Glu Ser Leu Val Lys Asn Pro Phe Pro Arg Ile Glu Asp  
 165 170 175

Glu Lys Phe Val Pro Glu Leu Tyr Ile Trp Asn Lys Ile Thr Asp Lys  
 180 185 190

Ala Lys Ile Arg Phe Asn Ile Ser Lys Val Ile Tyr Leu Cys Glu Tyr  
 195 200 205

Leu Asp Asp Gly Leu Ser Lys Asn Phe His Asn Gln Leu Lys Lys Tyr  
 210 215 220

Pro Lys Gly Phe Lys Ile Tyr Tyr Lys Asp Gln Arg Lys Arg Glu Lys  
 225 230 235 240

Thr Tyr Ile Lys Lys Thr Lys Met Leu Ile Arg Tyr Leu Gln Cys Cys  
 245 250 255

Tyr Tyr Glu Lys Ile  
 260

<210> 25

<211> 368

<212> PRT

<213> Escherichia coli

<400> 25

Met Lys Ile Leu Phe Val Ile Thr Gly Leu Gly Leu Gly Gly Ala Glu  
 1 5 10 15

Lys Gln Val Cys Leu Leu Ala Asp Lys Leu Ser Leu Ser Gly His His  
 20 25 30

Val Lys Ile Ile Ser Leu Gly His Met Ser Asn Asn Lys Val Phe Pro  
 35 40 45

Ser Glu Asn Asn Val Asn Val Ile Asn Val Asn Met Ser Lys Asn Ile  
 50 55 60

Ser Gly Val Ile Lys Gly Cys Val Arg Ile Arg Asp Val Ile Ala Asn  
 65 70 75 80

Phe Lys Pro Asp Ile Val His Ser His Met Phe His Ala Asn Ile Ile  
 85 90 95

Thr Arg Leu Ser Val Ile Gly Ile Lys Asn Arg Pro Gly Ile Ile Ser  
 100 105 110

Thr Ala His Asn Lys Asn Glu Gly Gly Tyr Phe Arg Met Leu Thr Tyr  
 115 120 125

Arg Ile Thr Asp Cys Leu Ser Asp Cys Cys Thr Asn Val Ser Lys Glu  
 130 135 140

Ala Val Asp Glu Phe Leu Arg Ile Lys Ala Phe Asn Pro Ala Lys Ala  
 145 150 155 160

Ile Thr Met Tyr Asn Gly Ile Asp Thr Asn Lys Phe Lys Phe Asp Leu  
                           165                          170                          175  
 Leu Ala Arg Arg Glu Ile Arg Asp Gly Ile Asn Ile Lys Asn Asp Asp  
                           180                          185                          190  
 Ile Leu Leu Leu Ala Ala Gly Arg Leu Thr Leu Ala Lys Asp Tyr Pro  
                           195                          200                          205  
 Asn Leu Leu Asn Ala Met Thr Leu Leu Pro Glu His Phe Lys Leu Ile  
                           210                          215                          220  
 Ile Ile Gly Asp Gly Glu Leu Arg Asp Glu Ile Asn Met Leu Ile Lys  
 225                          230                          235                          240  
 Lys Leu Gln Leu Ser Asn Arg Val Ser Leu Leu Gly Val Lys Lys Asn  
                           245                          250                          255  
 Ile Ala Pro Tyr Phe Ser Ala Cys Asp Ile Phe Val Leu Ser Ser Arg  
                           260                          265                          270  
 Trp Glu Gly Phe Gly Leu Val Val Ala Glu Ala Met Ser Cys Glu Arg  
                           275                          280                          285  
 Ile Val Val Gly Thr Asp Ser Gly Gly Val Arg Glu Val Ile Gly Asp  
                           290                          295                          300  
 Asp Asp Phe Leu Val Pro Ile Ser Asp Ser Thr Gln Leu Ala Ser Lys  
 305                          310                          315                          320  
 Ile Glu Lys Leu Ser Leu Ser Gln Ile Arg Asp His Ile Gly Phe Arg  
                           325                          330                          335  
 Asn Arg Glu Arg Ile Leu Lys Asn Phe Ser Ile Asp Thr Ile Ile Met  
                           340                          345                          350  
 Gln Trp Gln Glu Leu Tyr Gly Thr Ile Ile Cys Ser Lys His Glu Arg  
                           355                          360                          365

<210> 26

<211> 367

<212> PRT

<213> Escherichia coli

<400> 26

Met Thr Ala Arg Thr Thr Lys Val Leu His Leu Gln Leu Leu Pro Leu  
   1                          5                          10                          15  
 Leu Ser Gly Val Gln Arg Val Thr Leu Asn Glu Ile Ser Ala Leu Tyr  
                           20                          25                          30

Thr Asp Tyr Asp Tyr Thr Leu Val Cys Ser Lys Lys Gly Pro Leu Thr  
 35 40 45  
 Lys Ala Leu Leu Glu Tyr Asp Val Asp Cys His Cys Ile Pro Glu Leu  
 50 55 60  
 Thr Arg Glu Ile Thr Val Lys Asn Asp Phe Lys Ala Leu Phe Lys Leu  
 65 70 75 80  
 Tyr Lys Phe Ile Lys Lys Glu Lys Phe Asp Ile Val His Thr His Ser  
 85 90 95  
 Ser Lys Thr Gly Ile Leu Gly Arg Val Ala Ala Lys Leu Ala Arg Val  
 100 105 110  
 Gly Lys Val Ile His Thr Val His Gly Phe Ser Phe Pro Ala Ala Ser  
 115 120 125  
 Ser Lys Lys Ser Tyr Tyr Leu Tyr Phe Phe Met Glu Trp Ile Ala Lys  
 130 135 140  
 Phe Phe Thr Asp Lys Leu Ile Val Leu Asn Val Asp Asp Glu Tyr Ile  
 145 150 155 160  
 Ala Ile Asn Lys Leu Lys Phe Lys Arg Asp Lys Val Phe Leu Ile Pro  
 165 170 175  
 Asn Gly Val Asp Thr Asp Lys Phe Ser Pro Leu Glu Asn Lys Ile Tyr  
 180 185 190  
 Ser Ser Thr Leu Asn Leu Val Met Val Gly Arg Leu Ser Lys Gln Lys  
 195 200 205  
 Asp Pro Glu Thr Leu Leu Leu Ala Val Glu Lys Leu Leu Asn Glu Asn  
 210 215 220  
 Val Asn Val Lys Leu Thr Leu Val Gly Asp Gly Glu Leu Lys Glu Gln  
 225 230 235 240  
 Leu Glu Ser Arg Phe Lys Arg Gln Asp Gly Arg Ile Ile Phe His Gly  
 245 250 255  
 Trp Ser Asp Asn Ile Val Asn Ile Leu Lys Val Asn Asp Leu Phe Ile  
 260 265 270  
 Leu Pro Ser Leu Trp Glu Gly Met Pro Leu Ala Ile Leu Glu Ala Leu  
 275 280 285  
 Ser Cys Gly Leu Pro Cys Ile Val Thr Asn Ile Pro Gly Asn Asn Ser  
 290 295 300

Leu Ile Glu Asp Gly Tyr Asn Gly Cys Leu Phe Glu Ile Arg Asp Cys  
 305 310 315 320

Gln Leu Leu Ser Gln Lys Ile Met Ser Tyr Val Gly Lys Pro Glu Leu  
 325 330 335

Ile Ala Gln Gln Ser Thr Asn Ala Arg Ser Phe Ile Leu Lys Asn Tyr  
 340 345 350

Gly Leu Val Lys Arg Asn Asn Lys Val Arg Gln Leu Tyr Asp Asn  
 355 360 365

<210> 27

<211> 1272

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (319) .. (1269)

<220>

<221> CDS

<222> (3) .. (215)

<400> 27

cc ggg aag cac tcg gcg ctg att gtt gca cat cgt ctg acc acc gcg 47  
 Gly Lys His Ser Ala Leu Ile Val Ala His Arg Leu Thr Thr Ala  
 1 5 10 15

caa cgc tgc gat ctg att gcc gtt att gat aag ggg tta ctt gcg gaa 95  
 Gln Arg Cys Asp Leu Ile Ala Val Ile Asp Lys Gly Leu Leu Ala Glu  
 20 25 30

tac gga acc cac gaa cag ctg tta tct gcg ggc ggc ctc tat acc cgc 143  
 Tyr Gly Thr His Glu Gln Leu Leu Ser Ala Gly Gly Leu Tyr Thr Arg  
 35 40 45

tta tgg cat gac agc gtc agc agt act gct ctc cat cgc cag cac aac 191  
 Leu Trp His Asp Ser Val Ser Ser Thr Ala Leu His Arg Gln His Asn  
 50 55 60

atg aag gag gaa acc ccg gga tag ttactggaca cgtaatgtat taaaaacaca 245  
 Met Lys Glu Glu Thr Pro Gly  
 65 70

gtcagaagcg gcggtaccgt gaatagccgc tttaattatt tatactgaca tccttaattt 305

ttaaagagta tga atg ctg aac atg caa caa cat ctc tct gct atc gcc 354

Met Leu Asn Met Gln Gln His Leu Ser Ala Ile Ala																
75 80																
agc	ctg	cgc	aac	caa	ctg	gca	gcg	ggc	cac	att	gct	aac	ctt	act	gac	402
Ser	Leu	Arg	Asn	Gln	Leu	Ala	Ala	Gly	His	Ile	Ala	Asn	Leu	Thr	Asp	
85		90				95										
ttc	tgg	cgc	gaa	gct	gag	tcg	ctg	aat	gtt	cct	ctt	gtg	acg	cca	gtc	450
Phe	Trp	Arg	Glu	Ala	Glu	Ser	Leu	Asn	Val	Pro	Leu	Val	Thr	Pro	Val	
100		105				110				115						
gaa	gga	gcg	gaa	gat	gag	cga	gaa	gtg	acc	ttt	ctg	tgg	cgc	gcc	cga	498
Glu	Gly	Ala	Glu	Asp	Glu	Arg	Glu	Val	Thr	Phe	Leu	Trp	Arg	Ala	Arg	
120				125				130								
cat	cct	ctg	cag	ggc	gtt	tat	ctg	cgt	ctg	aac	cgg	gtg	acg	gat	aaa	546
His	Pro	Leu	Gln	Gly	Val	Tyr	Leu	Arg	Leu	Asn	Arg	Val	Thr	Asp	Lys	
135			140				145									
gag	cac	gta	gaa	aaa	gga	atg	atg	agc	gcc	ctt	ccc	gaa	acg	gat	atc	594
Glu	His	Val	Glu	Lys	Gly	Met	Met	Ser	Ala	Leu	Pro	Glu	Thr	Asp	Ile	
150			155				160									
tgg	aca	ctg	aca	ctg	cgt	tta	ccc	gca	agt	tac	tgc	ggc	tcc	tat	tcg	642
Trp	Thr	Leu	Thr	Leu	Arg	Leu	Pro	Ala	Ser	Tyr	Cys	Gly	Ser	Tyr	Ser	
165		170				175										
ctg	ctg	gaa	atc	ccc	ccc	ggc	act	acg	gct	gag	acg	att	gca	ctg	tcc	690
Leu	Leu	Glu	Ile	Pro	Pro	Gly	Thr	Thr	Ala	Glu	Thr	Ile	Ala	Leu	Ser	
180		185				190					195					
gga	ggc	cgt	ttt	gcc	acc	ctt	gcc	gga	aag	gcc	gat	ccg	cta	aac	aaa	738
Gly	Gly	Arg	Phe	Ala	Thr	Leu	Ala	Gly	Lys	Ala	Asp	Pro	Leu	Asn	Lys	
200				205				210								
atg	ccg	gag	atc	aac	gtt	cgg	gga	aac	gca	aag	gaa	tca	gtg	ctg	aca	786
Met	Pro	Glu	Ile	Asn	Val	Arg	Gly	Asn	Ala	Lys	Glu	Ser	Val	Leu	Thr	
215			220				225									
ctt	gat	aaa	gct	ccc	gcc	ctg	tcg	gaa	tgg	aac	ggc	ggc	ttc	cac	acc	834
Leu	Asp	Lys	Ala	Pro	Ala	Leu	Ser	Glu	Trp	Asn	Gly	Gly	Phe	His	Thr	
230			235				240									
gga	caa	ctg	ctt	acc	tcc	atg	cgc	att	atc	gcc	ggg	aaa	tct	cgc	cag	882
Gly	Gln	Leu	Leu	Thr	Ser	Met	Arg	Ile	Ile	Ala	Gly	Lys	Ser	Arg	Gln	
245		250				255										
gtt	cgg	ctc	tat	att	ccg	gat	gtt	gat	att	tct	cag	ccc	ctc	ggg	ctg	930
Val	Arg	Leu	Tyr	Ile	Pro	Asp	Val	Asp	Ile	Ser	Gln	Pro	Leu	Gly	Leu	
260		265				270					275					



gtc gtg ctg ccc gat ggt gaa acc tgg ttt gat cac ctt ggc gta tgc 978  
 Val Val Leu Pro Asp Gly Glu Thr Trp Phe Asp His Leu Gly Val Cys  
                   280                                  285                                  290

gcg gca att gac gcc gcc ata aat aat ggg cgc atc gtg ccc gtg gct 1026  
 Ala Ala Ile Asp Ala Ala Ile Asn Asn Gly Arg Ile Val Pro Val Ala  
                   295                                  300                                  305

gta ctg ggc att gac aac att aat gaa cat gaa cgc act gag ata ctc 1074  
 Val Leu Gly Ile Asp Asn Ile Asn Glu His Glu Arg Thr Glu Ile Leu  
                   310                                  315                                  320

ggc ggg cgc agc aaa ctg ata aag gat atc gcc gga cat ctg ctg ccg 1122  
 Gly Gly Arg Ser Lys Leu Ile Lys Asp Ile Ala Gly His Leu Leu Pro  
                   325                                  330                                  335

atg att cgc gct gaa caa ccg cag cgt cag tgg gca gac cgt tcg cgc 1170  
 Met Ile Arg Ala Glu Gln Pro Gln Arg Gln Trp Ala Asp Arg Ser Arg  
                   340                                  345                                  350                                  355

aca gtg ctg gcc ggg cag agc ctc ggc ggg atc agt gcg cta atg ggg 1218  
 Thr Val Leu Ala Gly Gln Ser Leu Gly Gly Ile Ser Ala Leu Met Gly  
                   360                                  365                                  370

gct cgt tac gca ccg gaa acg ttc ggt ctg gtg ctc agc cac tct cct 1266  
 Ala Arg Tyr Ala Pro Glu Thr Phe Gly Leu Val Leu Ser His Ser Pro  
                   375                                  380                                  385

caa tgc 1272  
 Gln

<210> 28

<211> 70

<212> PRT

<213> Escherichia coli

<400> 28

Gly Lys His Ser Ala Leu Ile Val Ala His Arg Leu Thr Thr Ala Gln  
   1                  5                                  10                                  15

Arg Cys Asp Leu Ile Ala Val Ile Asp Lys Gly Leu Leu Ala Glu Tyr  
                   20                                  25                                  30

Gly Thr His Glu Gln Leu Leu Ser Ala Gly Gly Leu Tyr Thr Arg Leu  
                   35                                  40                                  45

Trp His Asp Ser Val Ser Ser Thr Ala Leu His Arg Gln His Asn Met  
                   50                                  55                                  60

Lys Glu Glu Thr Pro Gly

65

70

&lt;210&gt; 29

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 29

```

Met Leu Asn Met Gln Gln His Leu Ser Ala Ile Ala Ser Leu Arg Asn
 1           5           10           15

Gln Leu Ala Ala Gly His Ile Ala Asn Leu Thr Asp Phe Trp Arg Glu
          20           25           30

Ala Glu Ser Leu Asn Val Pro Leu Val Thr Pro Val Glu Gly Ala Glu
          35           40           45

Asp Glu Arg Glu Val Thr Phe Leu Trp Arg Ala Arg His Pro Leu Gln
          50           55           60

Gly Val Tyr Leu Arg Leu Asn Arg Val Thr Asp Lys Glu His Val Glu
          65           70           75           80

Lys Gly Met Met Ser Ala Leu Pro Glu Thr Asp Ile Trp Thr Leu Thr
          85           90           95

Leu Arg Leu Pro Ala Ser Tyr Cys Gly Ser Tyr Ser Leu Leu Glu Ile
          100          105          110

Pro Pro Gly Thr Thr Ala Glu Thr Ile Ala Leu Ser Gly Gly Arg Phe
          115          120          125

Ala Thr Leu Ala Gly Lys Ala Asp Pro Leu Asn Lys Met Pro Glu Ile
          130          135          140

Asn Val Arg Gly Asn Ala Lys Glu Ser Val Leu Thr Leu Asp Lys Ala
          145          150          155          160

Pro Ala Leu Ser Glu Trp Asn Gly Gly Phe His Thr Gly Gln Leu Leu
          165          170          175

Thr Ser Met Arg Ile Ile Ala Gly Lys Ser Arg Gln Val Arg Leu Tyr
          180          185          190

Ile Pro Asp Val Asp Ile Ser Gln Pro Leu Gly Leu Val Val Leu Pro
          195          200          205

Asp Gly Glu Thr Trp Phe Asp His Leu Gly Val Cys Ala Ala Ile Asp
          210          215          220

```

Ala Ala Ile Asn Asn Gly Arg Ile Val Pro Val Ala Val Leu Gly Ile  
 225 230 235 240

Asp Asn Ile Asn Glu His Glu Arg Thr Glu Ile Leu Gly Gly Arg Ser  
 245 250 255

Lys Leu Ile Lys Asp Ile Ala Gly His Leu Leu Pro Met Ile Arg Ala  
 260 265 270

Glu Gln Pro Gln Arg Gln Trp Ala Asp Arg Ser Arg Thr Val Leu Ala  
 275 280 285

Gly Gln Ser Leu Gly Gly Ile Ser Ala Leu Met Gly Ala Arg Tyr Ala  
 290 295 300

Pro Glu Thr Phe Gly Leu Val Leu Ser His Ser Pro Gln  
 305 310 315

<210> 30

<211> 4039

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(285)

<220>

<221> CDS

<222> (370)..(1326)

<400> 30

cct tca atg tgg tgg acg cca gaa aga acc agt cga cca ggc ttg ttc 48  
 Pro Ser Met Trp Trp Thr Pro Glu Arg Thr Ser Arg Pro Gly Leu Phe  
 1 5 10 15

agc gaa acc gat acc tca tgg gtg agt gag cat ctg ctt tct gcc cca 96  
 Ser Glu Thr Asp Thr Ser Trp Val Ser Glu His Leu Leu Ser Ala Pro  
 20 25 30

ccg cag ggc gta cgt atc agc ctg tgc gtg gga tcg ctg gaa ggt tcg 144  
 Pro Gln Gly Val Arg Ile Ser Leu Cys Val Gly Ser Leu Glu Gly Ser  
 35 40 45

aca gtg cct cac gtt cag cag ctt cac cag cgg ctg att acc gct ggc 192  
 Thr Val Pro His Val Gln Gln Leu His Gln Arg Leu Ile Thr Ala Gly  
 50 55 60

gtc gaa agc cat tgc gca atc tac acc ggt ggt cac gat tac gca tgg 240

Val Glu Ser His Cys Ala Ile Tyr Thr Gly Gly His Asp Tyr Ala Trp  
 65 70 75 80  
 tgg cgc ggt gca ctg att gac ggg att ggt tta cta cag ggt tga 285  
 Trp Arg Gly Ala Leu Ile Asp Gly Ile Gly Leu Leu Gln Gly  
 85 90 95  
 gttgaccac aaacactttc aggaaacggt acagacttcc tgaataaatc aaatagtcac 345  
 ctgcggaaaaa ggaataatca tcag atg tat gcc cgc gag tat cgc tca aca 396  
 Met Tyr Ala Arg Glu Tyr Arg Ser Thr  
 100  
 cgc ccg cat aaa gcg att ttc ttt cat ctt tct tgc ctc acc ctt atc 444  
 Arg Pro His Lys Ala Ile Phe Phe His Leu Ser Cys Leu Thr Leu Ile  
 105 110 115 120  
 tgt agt gcg caa gtt tat gcg aag ccg gat atg cgg cca ctg ggg ccg 492  
 Cys Ser Ala Gln Val Tyr Ala Lys Pro Asp Met Arg Pro Leu Gly Pro  
 125 130 135  
 aat ata gcc gat aaa ggc tcc gtg ttt tac cat ttc agc gtc acc tct 540  
 Asn Ile Ala Asp Lys Gly Ser Val Phe Tyr His Phe Ser Val Thr Ser  
 140 145 150  
 ttc gac tct gtc gat ggc aca cgc cat tat cgg gta tgg acg gcc gtg 588  
 Phe Asp Ser Val Asp Gly Thr Arg His Tyr Arg Val Trp Thr Ala Val  
 155 160 165  
 ccg aat aca acc gca ccg gca tcc ggt tac ccg att tta tat atg ctt 636  
 Pro Asn Thr Thr Ala Pro Ala Ser Gly Tyr Pro Ile Leu Tyr Met Leu  
 170 175 180  
 gac ggt aac gca gtt atg gat cgc ctg gat gac gaa ctg ctc aaa caa 684  
 Asp Gly Asn Ala Val Met Asp Arg Leu Asp Asp Glu Leu Leu Lys Gln  
 185 190 195 200  
 ttg tca gaa aaa aca ccg cca gtg atc gtg gct gtc ggg tat cag acc 732  
 Leu Ser Glu Lys Thr Pro Pro Val Ile Val Ala Val Gly Tyr Gln Thr  
 205 210 215  
 aac ctc cct ttc gat ctc aac agc agg gct tac gac tat acg cca gca 780  
 Asn Leu Pro Phe Asp Leu Asn Ser Arg Ala Tyr Asp Tyr Thr Pro Ala  
 220 225 230  
 gca gaa agc aga aaa aca gat ctc cac tca ggg cgt ttt agc cgt aag 828  
 Ala Glu Ser Arg Lys Thr Asp Leu His Ser Gly Arg Phe Ser Arg Lys  
 235 240 245  
 agt ggt ggc agc aac aac ttc cgc cag tta ctg gaa acg cgt att gcc 876  
 Ser Gly Gly Ser Asn Asn Phe Arg Gln Leu Leu Glu Thr Arg Ile Ala

250	255	260	
cca aaa gtg gaa cag gga ctg aat atc gat cgg caa cgc cgc ggc tta			924
Pro Lys Val Glu Gln Gly Leu Asn Ile Asp Arg Gln Arg Arg Gly Leu			
265	270	275	280
tgg ggg cac tcc tac ggc ggc ctc ttc gtg ctg gat tcc tgg ctg tcc			972
Trp Gly His Ser Tyr Gly Gly Leu Phe Val Leu Asp Ser Trp Leu Ser			
	285	290	295
tcc tct tac ttc cgg tcg tac tac agc gcc agc ccg tcg ttg ggc aga			1020
Ser Ser Tyr Phe Arg Ser Tyr Tyr Ser Ala Ser Pro Ser Leu Gly Arg			
	300	305	310
ggt tat gat gct ttg cta agc cgc gtt acg gcg gtt gag cct ctg caa			1068
Gly Tyr Asp Ala Leu Leu Ser Arg Val Thr Ala Val Glu Pro Leu Gln			
	315	320	325
ttc tgc gcc aaa cac ctg gcg ata atg gaa ggc tcg gcg aca cag ggt			1116
Phe Cys Ala Lys His Leu Ala Ile Met Glu Gly Ser Ala Thr Gln Gly			
	330	335	340
gat aac cgg gaa acg cat gct gtc ggg gtg ctg tcg aaa att cat acc			1164
Asp Asn Arg Glu Thr His Ala Val Gly Val Leu Ser Lys Ile His Thr			
345	350	355	360
acc ctc act ata ctg aaa gat aaa ggc gtc aat gcc gta ttt tgg gat			1212
Thr Leu Thr Ile Leu Lys Asp Lys Gly Val Asn Ala Val Phe Trp Asp			
	365	370	375
ttc ccc aac ctg gga cac ggg ccg atg ttc aat gcc tcc ttt cgc cag			1260
Phe Pro Asn Leu Gly His Gly Pro Met Phe Asn Ala Ser Phe Arg Gln			
	380	385	390
gca ctg tta gat atc agt ggt gaa aac gca aat tac aca gca ggt tgt			1308
Ala Leu Leu Asp Ile Ser Gly Glu Asn Ala Asn Tyr Thr Ala Gly Cys			
	395	400	405
cat gag tta agc cac taa acactgcccg cttttacgcg ggcagtacgc			1356
His Glu Leu Ser His			
410			
ctgaaacact acgatcagaa tgatgcggta actccggcat agtaagcccg gcctggctcg			1416
ttataggtat tcgccccttc agaagatcgg aagatctggt tattgaggat attactgacg			1476
ccgacattaa gacgcagatt tttattaata tcgtaattga agttcgtccc caccagtgaa			1536
taagcgccca gctctttacc tgacagaccg ccagtatctt cactgcgggt ttccgcatga			1596
gtacgcgggt tttgtctgcc atataacgtc cagttgacgc tggcagaaaa cgctggggtg			1656

atggtccagt taagcgagtt attgatagta tatttcggga tgaccgacag aggattaccg 1716  
gtgtcttttt gctccgaagt gatcatccat gtggcattgg tattccagtt cagacgatct 1776  
ttcaccagtg ggaaagacat actggcttcg ataccgtcca ccagagcttt cccgccattc 1836  
tgccacttga ggatatatgc gcctgaagcg gtttgcccga taacgttatc cccggccacg 1896  
atcttattct ggtaatcatt gcggaagtag gtcacacttg cgtggtaatc ttcccagggtg 1956  
aactccagcc caatttcttt attgacgctg atttccggat cgagatcttt attaccgatc 2016  
aggtagcacc cgctgatgt aatatctttt ggacagccat tgcctttcga gtagagcaga 2076  
tagccttcac tggattgata caggtttggg gctttaaagg ttcgggcaac ccctgctttg 2136  
actttgaaat aatcgcccaa ttcctgcgaa agattcagac tggggctgaa gttcccgccg 2196  
gagtcgctga gataatcaaa gcgcaggccg ggaatgatat tcgtgccagg aaccggctca 2256  
atgttatctt caatatacag cgactgatt tgagaatgat ttttactgct gcgatccgca 2316  
gcagagccag aaataccgct gatatcactg tcattcaccg tcaggctggt agaggaagga 2376  
tcacgagct tatcgcggtt ccaactctgca ccaacggta gcgtttgatc aaccatcaca 2436  
ttcaaaggaa tattaagctc gccgctggtt cgccaggaac tcaggcgatt ggtcgtaaac 2496  
ttttcaccgg ctaaaatacg cccttcacca ccgccggata atccttcatt catgcgggta 2556  
ttattggttt tctcgtaata aacaccaaag cgactttgtc cccagtccca gataaccatta 2616  
tgcgtaatgc cataattctg tcggtacagg cggctcgtct cttgtgccgg attttgccag 2676  
gcttttcggt aactgcactg gaagaactgt tttgcgtatc gccgcataga tattcccctg 2736  
gcggctatat ccggcttcga aatcgagaat ctgctgcgga tttaatttcc acgagacaac 2796  
gccgttaata tctttgttac gtaccccttc atgcccggt gcgtttttcg taccgaccgg 2856  
agaattaata tcccaactgt cagcatccgt tttattcaga ttaccataca aacgctggt 2916  
aagagcatta ccagccagag gccactaag gctgaaattg gcgcgacgcg tagcgccctc 2976  
atcgctactt tccggctgat tgggtgataa cgacagcgaa ccgtgccagt cgttggtggg 3036  
acgtttggta atgatgttca ccaccccc ggctgcccc gaaccgtagc gcgccgccgc 3096  
agggccgcgg atcacttcaa tacgctcaac ctgttccggt ggcaccaggt tgggtgtcacc 3156  
gcgggtatca cgctctccac gccagctata acgcacggag ttacgtgacg tcaccggtac 3216

accatcaatt aaaattaagg tgttttccgg ccccatacca cgaatatcga tctggcggtt 3276  
 gttaccgcgt gtgcccagg cgctattgcc ggtaagattg acgccaggca ttttacgaat 3336  
 aatatctgaa aggtcgttta ccggaggggt ctttttaata tcctcgctgg taataaccga 3396  
 cacgcccggc tgctgtttta atacctgctc agcggtggtt tccaccacca gagtctcgtc 3456  
 attatcatcg tcggaggatt tggctactga tacctggcta ttcaacccaa ccaggagcac 3516  
 agttagcgac cagaggattt tgtaattct catacctatt ccctaataaa tgcctaactt 3576  
 aaaatgtttg atcgtaagc tcacatcctt gccagatatt ttttactgcc attattgttt 3636  
 ttatataaga atgataatta atatcattta gcaaaagaaa aagcaatccc tcacaagata 3696  
 aatatatcga tttttcataa atatcaaatt gatataaac atatgttttt tatttcattg 3756  
 tacttcagtc aaataaattt ctgaagcact gctagtagtg ccagttcagc tttctttttg 3816  
 actcattccg gcaaagtcag taccgttcat cttttgtact gatgttgcca ctggaaaatc 3876  
 ggtgcgcttg tcgatcatcg ggaattttgt cacaatttct aacggatagt gttcacattg 3936  
 tttctaacct gcattttcag acacggggcg tgcttatgta tataagatca gcatcactag 3996  
 gtctttctgc aacactactg ctttcaacaa ggtcaggcat ttc 4039

<210> 31

<211> 94

<212> PRT

<213> Escherichia coli

<400> 31

Pro Ser Met Trp Trp Thr Pro Glu Arg Thr Ser Arg Pro Gly Leu Phe  
           1                  5                  10                  15

Ser Glu Thr Asp Thr Ser Trp Val Ser Glu His Leu Leu Ser Ala Pro  
                   20                  25                  30

Pro Gln Gly Val Arg Ile Ser Leu Cys Val Gly Ser Leu Glu Gly Ser  
           35                  40                  45

Thr Val Pro His Val Gln Gln Leu His Gln Arg Leu Ile Thr Ala Gly  
           50                  55                  60

Val Glu Ser His Cys Ala Ile Tyr Thr Gly Gly His Asp Tyr Ala Trp  
           65                  70                  75                  80

Trp Arg Gly Ala Leu Ile Asp Gly Ile Gly Leu Leu Gln Gly

85

90

&lt;210&gt; 32

&lt;211&gt; 318

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 32

```

Met Tyr Ala Arg Glu Tyr Arg Ser Thr Arg Pro His Lys Ala Ile Phe
  1             5             10             15

Phe His Leu Ser Cys Leu Thr Leu Ile Cys Ser Ala Gln Val Tyr Ala
      20             25             30

Lys Pro Asp Met Arg Pro Leu Gly Pro Asn Ile Ala Asp Lys Gly Ser
      35             40             45

Val Phe Tyr His Phe Ser Val Thr Ser Phe Asp Ser Val Asp Gly Thr
      50             55             60

Arg His Tyr Arg Val Trp Thr Ala Val Pro Asn Thr Thr Ala Pro Ala
      65             70             75             80

Ser Gly Tyr Pro Ile Leu Tyr Met Leu Asp Gly Asn Ala Val Met Asp
      85             90             95

Arg Leu Asp Asp Glu Leu Leu Lys Gln Leu Ser Glu Lys Thr Pro Pro
      100            105            110

Val Ile Val Ala Val Gly Tyr Gln Thr Asn Leu Pro Phe Asp Leu Asn
      115            120            125

Ser Arg Ala Tyr Asp Tyr Thr Pro Ala Ala Glu Ser Arg Lys Thr Asp
      130            135            140

Leu His Ser Gly Arg Phe Ser Arg Lys Ser Gly Gly Ser Asn Asn Phe
      145            150            155            160

Arg Gln Leu Leu Glu Thr Arg Ile Ala Pro Lys Val Glu Gln Gly Leu
      165            170            175

Asn Ile Asp Arg Gln Arg Arg Gly Leu Trp Gly His Ser Tyr Gly Gly
      180            185            190

Leu Phe Val Leu Asp Ser Trp Leu Ser Ser Ser Tyr Phe Arg Ser Tyr
      195            200            205

Tyr Ser Ala Ser Pro Ser Leu Gly Arg Gly Tyr Asp Ala Leu Leu Ser
      210            215            220

```



Arg Val Thr Ala Val Glu Pro Leu Gln Phe Cys Ala Lys His Leu Ala  
 225 230 235 240  
 Ile Met Glu Gly Ser Ala Thr Gln Gly Asp Asn Arg Glu Thr His Ala  
 245 250 255  
 Val Gly Val Leu Ser Lys Ile His Thr Thr Leu Thr Ile Leu Lys Asp  
 260 265 270  
 Lys Gly Val Asn Ala Val Phe Trp Asp Phe Pro Asn Leu Gly His Gly  
 275 280 285  
 Pro Met Phe Asn Ala Ser Phe Arg Gln Ala Leu Leu Asp Ile Ser Gly  
 290 295 300  
 Glu Asn Ala Asn Tyr Thr Ala Gly Cys His Glu Leu Ser His  
 305 310 315

<210> 33

<211> 3292

<212> DNA

<213> Escherichia coli

<400> 33

ccgctgcggt tgattgccgg atgcggcgtg aacgccttat ccggcctaca atcattgcaa 60  
 attcaataaa ttgcagcggt ctgtaggctg gataagatgc gtcagcatcg catccggcaa 120  
 aggcatatct cagcgatagc gccggcttag tcagatttaa tctgcgcgcg tgggtggatat 180  
 tttttcagga tctccatata cgcggtgcatt tcgggtctgta gcggtacacc catcggaata 240  
 tggcgacacg cgatagagtc gctttcctgc ggatcgggtg acagggttaa caccgacgat 300  
 cccgccgttt gcattactgt gccgggtgaat ccaccctgat atccgctctg ggtataagcg 360  
 taagggttgc gaatcaggac gtgatacttg aactcatcca tacgcacagc agaaagttaa 420  
 ccgttgagga agtagtgctc ggccttacgg ttagactgac catttggttc caggaagaaa 480  
 gatgtctggt ccacaccatc gataaagggt gttttcggta cttaaattcgc tactttcgcc 540  
 ccaggatgcc ccgccagatc cagcgccgta gggaagagat ccgccagatc gacaatgccg 600  
 tcagatttac gcggttggtat catgcctttc cagtaaacga aggttggcac acgaacgccg 660  
 ctttcccatg tagaaccttt cgcaccgcgg aacggcgtgc gaccgtgcgg cggaacttcg 720  
 gcttcgcgac cgttatcaga ggtgaacaca atcagcgtgt tatcaagctg accgtttttc 780  
 tccagtgcct tatacagatt ggcgaagata tcgttcatct ccaccatgca gtcgccgtaa 840  
 gaggtgcgcg ccggagagct acccgcatat ttggcggttc ggtagttatc gaagtgcagc 900  
 ccgcgagtg cgtaatagag gaagaaaggc ttatcactct tcgccatctt gtcgaggaac 960  
 ttaacgccat attccatcca gcgttgatcc aggtcttcca tatatttcgg cgtaatgtcg 1020  
 gcaatggctt cctgttcacc gccgcgcacg gcatgaacgt catctttgct gaacggcagt 1080  
 ttttgatgt attcagaacg agccgggctc agggcgactt ccgggttgac atgaacatca 1140  
 cgccattcgg tatacatatc ggacaccgag ttaaagccgc ggaaatcatc aaagccaacg 1200  
 ttctgcggct gcgactcttt gttttcccc atatgccatt tcccgatagc ctgggtgacg 1260  
 tagccctgat cgtgcagcaa ctgcggcagc gtggttaacc cttgcagacc gcccggttgc 1320  
 ccgtacattg gcggcatcag aatgccgtgg tggatggagt attgtccggt gagaatcgtg 1380  
 gcgcgggttg gggagaact cggttgagaa tacgccgaag ttaaaatcag cccctggctg 1440  
 gcaacggcgt cgatatctgg tgtagggtta cccaccgcca cgccgccgcc gttaaagcca 1500

```

acgtccatcc agccacatc atccagcaag aaaacaacca cgttcggttt cttaccgggt 1560
tttttctcaa gttccgccag tttctgctgg gtttctttgt cttgtgcagg atgctgcatc 1620
accggcatca tgttgctggc aatagtgggc gccggtttta ccagatactg gtttggtga 1680
tcgtatccgg caaagccttt gcgtgcggtg gcggttgacg gggatctgc tgcgctggct 1740
atgagaggaa gagctgcggc gacagcaaca acaagaagtt tgggtgaaaa cgaaaattcc 1800
atgcaaaatg ctccggtttc atgtcgtcaa aatgatgacg taattaagca ttgataattg 1860
agatccctct ccctgacagg atgattgcat aaataatagt gataaaaata aattatttat 1920
ttatccagaa atgaattgaa aaatcaggag agcattttca atcctacctc tggcgcagg 1980
gatattgtaa ggcggtgatg ttatatcgcg ttgattattg atgctgtttt tagttttaac 2040
ggcattaata tatatgttat taattgaatg acttttatta ttcattatat atatgtgtag 2100
aattgtgcgc aggagaaata ttcactcagg aagttattac tcaggaagca aagaggatta 2160
cagaattatc tcataacaag tgtaaaggga tgttatttcc cggttctctg tggcataata 2220
aacgagtaga tgcctattcc atctcttatg ttgccttag tgcctcataa actccggaat 2280
gacgcagagc cgtttacggg gcttatcgtc cactgacaga tgctgcttat gcctcatcag 2340
acaccatgga cacaacgttg agtgaagcac ccacttggtg tcatacagac ctgttttaac 2400
gcctgctccg taataagagc aggcgttttt ttatatatca gaaaggcccc ggagggtgctt 2460
gcctccgggt gagaaagagc tactgtggcg gggtgttctg caacgttaac atcaaaccgt 2520
cgcgacgcat cgtgcgggt tcttccggct tgtgcagtct gtccagcgcg tcggcaagcc 2580
atgcgtaatc gtaggcgtcc ggacgttggt tcagcgctgc gcggaaggcg agcgatgctt 2640
cctgccattc tccgtgtttc atcagcgact gaccagtggt gctccacaac agcgggcgat 2700
cgcccacgtt tttgatctgt tggcgcagca ctttttccaa gctgttcccg ggtaattgg 2760
gttttcagac gccggggatc ggcagcagca ggccgaatcg tcatactggc gtttcaggcc 2820
atcgatgata atttgctggg cagtatcatg atcgtcacac tcaataagat gttccgccat 2880
tgccacctgc aaggccacct gatgacgcgt tttccggctt tggtttttcc accagttacg 2940
caaaccttca ctaccgttat cggcacgcgc ctgatccatc aggccaatcc atgcctgttg 3000
ttccagcatt gcacgatgtt cttcatcacc aacatgggct ttcgccattg atgggatgat 3060
atccagcagc gaactccatg caccagtgcg gatatacgcc tgttccgcca gacgtaatac 3120
ttccggatgg cgtggcgtaa cttccagcag cttatccacg ccgtgacgtg ctgcatgggt 3180
ttcattacgg gccagttgca gacgtacacg ggtgatttct accggaatgg tgtcattgcc 3240
ggccagctcc gctgcgcggt ccagatgttg gttggcgcgt gcttcagcat cc 3292

```

```

<210> 34
<211> 11165
<212> DNA
<213> Escherichia coli

```

```

<220>
<221> CDS
<222> (3791)..(4834)

<220>
<221> CDS
<222> (10459)..(10776)

```

```

<220>
<221> CDS
<222> (10134)..(10427)

```

```

<220>
<221> CDS

```

<222> (9836) .. (10081)

<220>

<221> CDS

<222> (7816) .. (9480)

<220>

<221> CDS

<222> (4878) .. (7802)

<220>

<221> CDS

<222> (3460) .. (3702)

<220>

<221> CDS

<222> (3054) .. (3407)

<220>

<221> CDS

<222> (2613) .. (3041)

<220>

<221> CDS

<222> (2198) .. (2530)

<220>

<221> CDS

<222> (1939) .. (2196)

<220>

<221> CDS

<222> (1573) .. (1893)

<220>

<221> CDS

<222> (1102) .. (1485)

<220>

<221> CDS

<222> (2) .. (1099)

<400> 34

c agc gat atg cag cgc ggt atc cag gct gca acg gct gca ctt cag ggc 49  
 Ser Asp Met Gln Arg Gly Ile Gln Ala Ala Thr Ala Ala Leu Gln Gly  
           1                  5                  10                  15

ctg gtg ggc ggc aat atg gca ggc gcg ctg gca ggt gct tca gcg ccg 97  
 Leu Val Gly Gly Asn Met Ala Gly Ala Leu Ala Gly Ala Ser Ala Pro  
                   20                  25                  30

gag ctg gcg aac atc atc ggt cat cac gcg ggt att gat gac aat aca	145
Glu Leu Ala Asn Ile Ile Gly His His Ala Gly Ile Asp Asp Asn Thr	
35 40 45	
gcg gca aaa gcc att gcc cat gcc att ctc ggt ggt gtg aca gca gcc	193
Ala Ala Lys Ala Ile Ala His Ala Ile Leu Gly Gly Val Thr Ala Ala	
50 55 60	
ctt cag ggc aac agt gcg gca gca ggc gca att ggt gcg ggt act ggt	241
Leu Gln Gly Asn Ser Ala Ala Ala Gly Ala Ile Gly Ala Gly Thr Gly	
65 70 75 80	
gaa gtg atc gcg tca gcc att gcg aaa agc ctc tac ccg ggc gta gat	289
Glu Val Ile Ala Ser Ala Ile Ala Lys Ser Leu Tyr Pro Gly Val Asp	
85 90 95	
ccg tcg aaa ctg aca gaa gat cag aag caa act gta agc acg ctg gca	337
Pro Ser Lys Leu Thr Glu Asp Gln Lys Gln Thr Val Ser Thr Leu Ala	
100 105 110	
acg ctg tca gcg ggt atg gcc ggc ggc att gcc agt ggc gat gtg gct	385
Thr Leu Ser Ala Gly Met Ala Gly Gly Ile Ala Ser Gly Asp Val Ala	
115 120 125	
ggc gcg gct gct gga gct ggt gcc ggg aag aac gtt gtt gag aat aat	433
Gly Ala Ala Ala Gly Ala Gly Ala Gly Lys Asn Val Val Glu Asn Asn	
130 135 140	
gcg ctg agt ctg gtt gcc aga ggc tgt gcg gtc gca gca cct tgc agg	481
Ala Leu Ser Leu Val Ala Arg Gly Cys Ala Val Ala Ala Pro Cys Arg	
145 150 155 160	
act aaa gtt gca gag cag ttg cta gaa atc ggg gcg aaa gcg ggc atg	529
Thr Lys Val Ala Glu Gln Leu Leu Glu Ile Gly Ala Lys Ala Gly Met	
165 170 175	
gcc ggg ctt gcc ggg gcg gca gtc aag gat atg gcc gac agg atg acc	577
Ala Gly Leu Ala Gly Ala Ala Val Lys Asp Met Ala Asp Arg Met Thr	
180 185 190	
tcc gat gaa ctg gag cat ctg att acc ctg caa atg atg ggt aat gat	625
Ser Asp Glu Leu Glu His Leu Ile Thr Leu Gln Met Met Gly Asn Asp	
195 200 205	
gag atc act act aag tat ctc agt tcg ttg cat gat aag tac ggt tcc	673
Glu Ile Thr Thr Lys Tyr Leu Ser Ser Leu His Asp Lys Tyr Gly Ser	
210 215 220	
ggg gct gcc tcg aat ccg aat atc ggt aaa gat ctg acc gat gcg gaa	721
Gly Ala Ala Ser Asn Pro Asn Ile Gly Lys Asp Leu Thr Asp Ala Glu	
225 230 235 240	

aaa gta gaa ctg ggc ggt tcc ggc tca gga acc ggt aca cca cca cca	769
Lys Val Glu Leu Gly Gly Ser Gly Ser Gly Thr Gly Thr Pro Pro Pro	
245 250 255	
tcg gaa aat gat cct aag cag caa aat gaa aaa act gta gat aag ctt	817
Ser Glu Asn Asp Pro Lys Gln Gln Asn Glu Lys Thr Val Asp Lys Leu	
260 265 270	
aat cag aag caa gaa agt gcg att aag aag atc gat aac act ata aaa	865
Asn Gln Lys Gln Glu Ser Ala Ile Lys Lys Ile Asp Asn Thr Ile Lys	
275 280 285	
aat gct ctg aaa gat cat gat att att gga act ctc aag gat atg gat	913
Asn Ala Leu Lys Asp His Asp Ile Ile Gly Thr Leu Lys Asp Met Asp	
290 295 300	
ggg aag cca gtt cct aaa gag aat gga gga tat tgg gat cat atg cag	961
Gly Lys Pro Val Pro Lys Glu Asn Gly Gly Tyr Trp Asp His Met Gln	
305 310 315 320	
gaa atg caa aat acg ctc aga gga tta aga aat cat gcg gat acg ttg	1009
Glu Met Gln Asn Thr Leu Arg Gly Leu Arg Asn His Ala Asp Thr Leu	
325 330 335	
aaa aac gtc aac aat cct gaa gct cag gct gcg tat ggc aga gca aca	1057
Lys Asn Val Asn Asn Pro Glu Ala Gln Ala Ala Tyr Gly Arg Ala Thr	
340 345 350	
gat gct att aat aaa ata gaa tca gcc ttg aaa gga tat gga at atg	1104
Asp Ala Ile Asn Lys Ile Glu Ser Ala Leu Lys Gly Tyr Gly Met	
355 360 365	
att acc tta cgt aaa ttg att gga aac atc aat atg aca aaa gag cct	1152
Ile Thr Leu Arg Lys Leu Ile Gly Asn Ile Asn Met Thr Lys Glu Pro	
370 375 380	
gag caa caa tca ccg ctt gaa ctc tgg ttc gaa cgt atc ata gat gtg	1200
Glu Gln Gln Ser Pro Leu Glu Leu Trp Phe Glu Arg Ile Ile Asp Val	
385 390 395	
cct ctt gaa aag tta aca gtg gaa gat ctt tgc cgc gct atc cga caa	1248
Pro Leu Glu Lys Leu Thr Val Glu Asp Leu Cys Arg Ala Ile Arg Gln	
400 405 410 415	
aat tta tgt att gat cag ttg atg cca aga gtg ttg gaa gtt cta act	1296
Asn Leu Cys Ile Asp Gln Leu Met Pro Arg Val Leu Glu Val Leu Thr	
420 425 430	
aaa gag ccg tta gcg ggt gaa tat tac gat ggt gaa cta att gca gct	1344
Lys Glu Pro Leu Ala Gly Glu Tyr Tyr Asp Gly Glu Leu Ile Ala Ala	
435 440 445	

tta tca acg ata aaa gga gaa gat cta aaa gat cag aaa agt acc ttt 1392  
 Leu Ser Thr Ile Lys Gly Glu Asp Leu Lys Asp Gln Lys Ser Thr Phe  
           450                          455                          460

acc caa ata agg caa ctt ata aac cag cta gaa ccg tca gat att aac 1440  
 Thr Gln Ile Arg Gln Leu Ile Asn Gln Leu Glu Pro Ser Asp Ile Asn  
           465                          470                          475

gat gat tta aga aaa gat ata tta aaa atc aat cag ata att gta 1485  
 Asp Asp Leu Arg Lys Asp Ile Leu Lys Ile Asn Gln Ile Ile Val  
 480                          485                          490

taactaatcc cggccactga gccgagatct tctttgtgtg ccgggcatgt tcagcagctt 1545

gggggtgaaa gtccctgtc cagcctg atg gtg gcg aag gcg ttc gcg tac gca 1599  
                                   Met Val Ala Lys Ala Phe Ala Tyr Ala  
                                   495                                  500

ctt aac cag tgg ccg gca ctg acg tac tat gcg aac gat ggc tgg gtg 1647  
 Leu Asn Gln Trp Pro Ala Leu Thr Tyr Tyr Ala Asn Asp Gly Trp Val  
           505                          510                          515

gaa atc gac aac aac atc gct gaa aat gcc ctg cgg gcg gtc agt ctg 1695  
 Glu Ile Asp Asn Asn Ile Ala Glu Asn Ala Leu Arg Ala Val Ser Leu  
 520                          525                          530                          535

ggg cgt aaa aac ttc ctg ttc ttc ggc tct gac cat ggt ggt gag cgg 1743  
 Gly Arg Lys Asn Phe Leu Phe Phe Gly Ser Asp His Gly Gly Glu Arg  
                           540                          545                          550

gga gcg cta ctg tac agc ctg atc ggg acg tgc aaa ctg aat gac gtg 1791  
 Gly Ala Leu Leu Tyr Ser Leu Ile Gly Thr Cys Lys Leu Asn Asp Val  
           555                          560                          565

gat cca gaa agc tac ctt cgc cat gtg ctt gcc gtc ata gca gac tgg 1839  
 Asp Pro Glu Ser Tyr Leu Arg His Val Leu Ala Val Ile Ala Asp Trp  
           570                          575                          580

ccg gtc aac cgg gtc agc gaa ctg ctt ccg tgg cgc ata gca ctg cca 1887  
 Pro Val Asn Arg Val Ser Glu Leu Leu Pro Trp Arg Ile Ala Leu Pro  
           585                          590                          595

gct gaa taacacatcc ccgtcaatac ggccctcgct gtacgcttag agaaa atg ctg 1944  
 Ala Glu  Met Leu  
 600

atg tct gta cag aaa gaa aag aac gtc gca gag agt gtg gta tct gaa 1992  
 Met Ser Val Gln Lys Glu Lys Asn Val Ala Glu Ser Val Val Ser Glu  
           605                          610                          615

acg cat acc ggc gac agc gta tat gct tcc ctg ttt gaa aaa att aac 2040

Thr His Thr Gly Asp Ser Val Tyr Ala Ser Leu Phe Glu Lys Ile Asn	
620	625 630 635
ctg aat ccg gta tct gcc ctg agt gca ctg gat aac cct ttc cgg tca	2088
Leu Asn Pro Val Ser Ala Leu Ser Ala Leu Asp Asn Pro Phe Arg Ser	
	640 645 650
gca gat aac gcg act ggc aga att acc tcc agc ata caa cct gcg gtg	2136
Ala Asp Asn Ala Thr Gly Arg Ile Thr Ser Ser Ile Gln Pro Ala Val	
	655 660 665
cag tgc gca gct gct gca gca act gag ggt tct tgt ccc cgg caa tcc	2184
Gln Cys Ala Ala Ala Ala Ala Thr Glu Gly Ser Cys Pro Arg Gln Ser	
	670 675 680
ccg tgt tca gga a atg gtg gat aac tgg cag aag agt gta agg agt cgt	2233
Pro Cys Ser Gly Met Val Asp Asn Trp Gln Lys Ser Val Arg Ser Arg	
	685 690 695
gcg ctc ccg gaa gag gcg atg acg ggc tgg aac gaa ggc atg atc cgc	2281
Ala Leu Pro Glu Glu Ala Met Thr Gly Trp Asn Glu Gly Met Ile Arg	
	700 705 710 715
tta cag cag ttg gct gag cgc ctg aac cgt cag gat gaa cag cgg gga	2329
Leu Gln Gln Leu Ala Glu Arg Leu Asn Arg Gln Asp Glu Gln Arg Gly	
	720 725 730
aaa tac atg acg gtc agt gaa ctg aaa acg gag gtg ttt ggc atc atg	2377
Lys Tyr Met Thr Val Ser Glu Leu Lys Thr Glu Val Phe Gly Ile Met	
	735 740 745
cag gct ttt aac cgg cat atc ccg gcg gaa gag cag tta cgt cgc tac	2425
Gln Ala Phe Asn Arg His Ile Pro Ala Glu Glu Gln Leu Arg Arg Tyr	
	750 755 760
ggt gaa gtc cgt aac cag aat ggc agt gaa cag cag caa aaa cag gct	2473
Gly Glu Val Arg Asn Gln Asn Gly Ser Glu Gln Gln Gln Lys Gln Ala	
	765 770 775
gaa atg gcg cta aat cag tta att aac cgt tat cag atg ata cgt gca	2521
Glu Met Ala Leu Asn Gln Leu Ile Asn Arg Tyr Gln Met Ile Arg Ala	
	780 785 790 795
ggc aaa caa tagtggtagc cataatgcag gagcaaagcc tgaatcagga	2570
Gly Lys Gln	
agagttattc tgactgagtt tgggttttctg gcgattcttg tg atg gtg gga tgt	2624
	Met Val Gly Cys
	800
gct tgg tta gct gaa cag gcc ttt tcc gac cat gcg ctt tca cca cac	2672

Ala	Trp	Leu	Ala	Glu	Gln	Ala	Phe	Ser	Asp	His	Ala	Leu	Ser	Pro	His		
		805					810					815					
agt	gct	tgg	ccg	tac	agt	gca	tcg	cgc	gat	gcc	ggg	ctg	gcc	gat	acg	2720	
Ser	Ala	Trp	Pro	Tyr	Ser	Ala	Ser	Arg	Asp	Ala	Gly	Leu	Ala	Asp	Thr		
		820				825					830						
ggc	gcg	ggc	ggc	tat	ccc	act	tgt	aaa	cag	cgg	tgg	gcc	gac	gac	acc	2768	
Gly	Ala	Gly	Gly	Tyr	Pro	Thr	Cys	Lys	Gln	Arg	Trp	Ala	Asp	Asp	Thr		
		835			840				845						850		
ggt	ggg	ctg	aaa	gcc	cgt	cta	ctg	caa	ctt	cct	gcc	cta	gat	atc	tgg	2816	
Val	Gly	Leu	Lys	Ala	Arg	Leu	Leu	Gln	Leu	Pro	Ala	Leu	Asp	Ile	Trp		
				855				860						865			
acg	gcg	ttt	aaa	aaa	atc	gac	cag	tcg	cag	gta	gtg	tat	gaa	gag	gcc	2864	
Thr	Ala	Phe	Lys	Lys	Ile	Asp	Gln	Ser	Gln	Val	Val	Tyr	Glu	Glu	Ala		
			870				875						880				
gtg	ctg	cgc	tcg	cgg	gtc	agt	gaa	cga	aat	atg	cag	gta	tcg	cag	aat	2912	
Val	Leu	Arg	Ser	Arg	Val	Ser	Glu	Arg	Asn	Met	Gln	Val	Ser	Gln	Asn		
		885					890					895					
ggg	cgc	ggt	tat	cca	agc	tat	ggc	ggt	aac	ggt	gat	ggc	acc	gtc	gcc	2960	
Gly	Arg	Val	Tyr	Pro	Ser	Tyr	Gly	Gly	Asn	Val	Asp	Gly	Thr	Val	Ala		
		900				905					910						
aat	gcc	gcc	acc	cgg	ttg	gca	tcc	ggc	gct	aga	aat	atc	ctc	ggc	agc	3008	
Asn	Ala	Ala	Thr	Arg	Leu	Ala	Ser	Gly	Ala	Arg	Asn	Ile	Leu	Gly	Ser		
		915			920				925					930			
ata	gcg	gca	tgt	acg	gca	ttc	gac	agc	gtg	cgt	taggcactac	cg	atg	gta	3059		
Ile	Ala	Ala	Cys	Thr	Ala	Phe	Asp	Ser	Val	Arg			Met	Val			
				935				940									
cag	gcg	cag	ctg	caa	ata	gcg	ctg	gtg	atc	tgt	att	ccg	ctg	ata	acg	3107	
Gln	Ala	Gln	Leu	Gln	Ile	Ala	Leu	Val	Ile	Cys	Ile	Pro	Leu	Ile	Thr		
		945				950					955						
ctc	tgt	tcg	gcg	tgg	gat	gtg	aaa	gta	gtg	atg	acg	ctg	acg	ttt	gtg	3155	
Leu	Cys	Ser	Ala	Trp	Asp	Val	Lys	Val	Val	Met	Thr	Leu	Thr	Phe	Val		
		960			965				970					975			
cag	ttt	gca	cta	ttt	ttc	ctc	acc	ttt	tgg	tgg	gaa	ctg	gca	cgg	tgg	3203	
Gln	Phe	Ala	Leu	Phe	Phe	Leu	Thr	Phe	Trp	Trp	Glu	Leu	Ala	Arg	Trp		
				980				985						990			
ctt	gat	agc	tgg	ctg	ctg	gat	gtg	ctc	tac	aac	agc	gat	acc	cac	agt	3251	
Leu	Asp	Ser	Trp	Leu	Leu	Asp	Val	Leu	Tyr	Asn	Ser	Asp	Thr	His	Ser		
			995				1000						1005				



agc tgg aat tta gcc ggg atc cag aat acg cag gat gac gtg att atc 3299  
 Ser Trp Asn Leu Ala Gly Ile Gln Asn Thr Gln Asp Asp Val Ile Ile  
 1010 1015 1020

aat ctg gtg atg agg ttg atg ttt ctg gtg ttg ccg aca ttc tgg ctg 3347  
 Asn Leu Val Met Arg Leu Met Phe Leu Val Leu Pro Thr Phe Trp Leu  
 1025 1030 1035

ggg gcg atg acg tgg gct gga gtg agg gtt ggc gtg gcg ctg aat gga 3395  
 Gly Ala Met Thr Trp Ala Gly Val Arg Val Gly Val Ala Leu Asn Gly  
 1040 1045 1050 1055

gcg ctg gcg gga tgattgggag gtgattcgcc aatctcactt tcctatacac 3447  
 Ala Leu Ala Gly

atataaaatg ta atg aaa tat ctc ttt ttt gag aat ata cat tct ata ttt 3498  
 Met Lys Tyr Leu Phe Phe Glu Asn Ile His Ser Ile Phe  
 1060 1065 1070

tta aca ttc agt ctc ttc cga aca tct gtg tcg cct gat ttc cca atg 3546  
 Leu Thr Phe Ser Leu Phe Arg Thr Ser Val Ser Pro Asp Phe Pro Met  
 1075 1080 1085

att ttt gca ttg ccc tca atc att tta ggt caa ttt acg acc aac caa 3594  
 Ile Phe Ala Leu Pro Ser Ile Ile Leu Gly Gln Phe Thr Thr Asn Gln  
 1090 1095 1100

tta act aac ttt gtg ata tgt atg ggt aac acc gtt gaa cgt cgg ctg 3642  
 Leu Thr Asn Phe Val Ile Cys Met Gly Asn Thr Val Glu Arg Arg Leu  
 1105 1110 1115 1120

ggt gtt gtt cat aat ccc ttt aaa agg tct ggg gat ggc cat gac ctc 3690  
 Gly Val Val His Asn Pro Phe Lys Arg Ser Gly Asp Gly His Asp Leu  
 1125 1130 1135

agg gcg gta gcg tgaccaaagt tcatatccat accaattatt tttattttaa 3742  
 Arg Ala Val Ala  
 1140

atatcaactt attcgagttg ttttatttag ttcaaagaag gtatcaaa ttg ata gtt 3799  
 Leu Ile Val

ata gat ttt ttt tgt ggc tgt ggt gga gcc agt gaa ggg cta cgt cag 3847  
 Ile Asp Phe Phe Cys Gly Cys Gly Gly Ala Ser Glu Gly Leu Arg Gln  
 1145 1150 1155

gct ggc ttt gat atc gag ctt gga tta gat att gac caa caa gca tca 3895  
 Ala Gly Phe Asp Ile Glu Leu Gly Leu Asp Ile Asp Gln Gln Ala Ser  
 1160 1165 1170 1175

gaa aca ttt aaa gct aat ttc cct gat gca aaa ttc atc caa gat gat 3943

Glu Thr Phe Lys Ala Asn Phe Pro Asp Ala Lys Phe Ile Gln Asp Asp	
1180 1185 1190	
att agg aaa atc gaa cct caa gat atc tcc gac atc att gat att aaa	3991
Ile Arg Lys Ile Glu Pro Gln Asp Ile Ser Asp Ile Ile Asp Ile Lys	
1195 1200 1205	
gct aaa cgg cct ttg tta ctg agt gca tgt gca cca tgt caa cca ttt	4039
Ala Lys Arg Pro Leu Leu Leu Ser Ala Cys Ala Pro Cys Gln Pro Phe	
1210 1215 1220	
tcg caa cag aat aaa aat aaa act agt gac gac tca agg aga aat cta	4087
Ser Gln Gln Asn Lys Asn Lys Thr Ser Asp Asp Ser Arg Arg Asn Leu	
1225 1230 1235	
cta aat gaa act cat cgt ttt att aga gaa ctt ctt cct gaa tat att	4135
Leu Asn Glu Thr His Arg Phe Ile Arg Glu Leu Leu Pro Glu Tyr Ile	
1240 1245 1250 1255	
atg ctt gaa aat gtt cct gga atg caa aaa att gat gaa gaa aaa gaa	4183
Met Leu Glu Asn Val Pro Gly Met Gln Lys Ile Asp Glu Glu Lys Glu	
1260 1265 1270	
ggc cca ttt cag gag ttt att aag cta ctt aaa gag tta gag tat aac	4231
Gly Pro Phe Gln Glu Phe Ile Lys Leu Leu Lys Glu Leu Glu Tyr Asn	
1275 1280 1285	
tat ata tct ttt ata gcc aat gct gag aac tat ggg att ccc caa aga	4279
Tyr Ile Ser Phe Ile Ala Asn Ala Glu Asn Tyr Gly Ile Pro Gln Arg	
1290 1295 1300	
aga aaa aga ctc gtg ctc tta gct agt cga gta ggt aaa gtt acc cta	4327
Arg Lys Arg Leu Val Leu Leu Ala Ser Arg Val Gly Lys Val Thr Leu	
1305 1310 1315	
cca gag ata acc cat ggt aaa aat aaa atc cca ttc aaa act gta cga	4375
Pro Glu Ile Thr His Gly Lys Asn Lys Ile Pro Phe Lys Thr Val Arg	
1320 1325 1330 1335	
gat tat atc cag gac ttc aca aag tta tgt tca gga gaa acc gac ccc	4423
Asp Tyr Ile Gln Asp Phe Thr Lys Leu Cys Ser Gly Glu Thr Asp Pro	
1340 1345 1350	
aaa gat cct tta cat agg gct gga aca ctg agc cct ctt aac cta aaa	4471
Lys Asp Pro Leu His Arg Ala Gly Thr Leu Ser Pro Leu Asn Leu Lys	
1355 1360 1365	
aga att atg cac act cca gaa gga ggg gat aga aga aat tgg cca gaa	4519
Arg Ile Met His Thr Pro Glu Gly Gly Asp Arg Arg Asn Trp Pro Glu	
1370 1375 1380	

gag tta gtt aat aaa tgc cat aaa aat tat gat ggc cac aca gat act 4567  
 Glu Leu Val Asn Lys Cys His Lys Asn Tyr Asp Gly His Thr Asp Thr  
 1385 1390 1395

tat gga aga atg agt tgg gat aag cct gcg cct aca ctt acg acg aaa 4615  
 Tyr Gly Arg Met Ser Trp Asp Lys Pro Ala Pro Thr Leu Thr Thr Lys  
 1400 1405 1410 1415

tgt aat agt tac tcc aat ggt cgt ttt ggg cat cct gac ccc act caa 4663  
 Cys Asn Ser Tyr Ser Asn Gly Arg Phe Gly His Pro Asp Pro Thr Gln  
 1420 1425 1430

cat aga gca att agc ata aga gaa gca tca aga tta caa aca ttt cct 4711  
 His Arg Ala Ile Ser Ile Arg Glu Ala Ser Arg Leu Gln Thr Phe Pro  
 1435 1440 1445

tta agc tat gtt ttt aaa ggt tcg ctg aat tca atg gca aag caa atc 4759  
 Leu Ser Tyr Val Phe Lys Gly Ser Leu Asn Ser Met Ala Lys Gln Ile  
 1450 1455 1460

ggc aat gct gta cct tgc gaa ctc gct aga cta ttt ggg cta cat ctc 4807  
 Gly Asn Ala Val Pro Cys Glu Leu Ala Arg Leu Phe Gly Leu His Leu  
 1465 1470 1475

ata gaa aat tgt act aat aag gat tca tagatatatg gctaaaataa 4854  
 Ile Glu Asn Cys Thr Asn Lys Asp Ser  
 1480 1485

gaacaaaggc tcgagctttg gac atg ctt ggc aga caa caa att gca ggt ata 4907  
 Met Leu Gly Arg Gln Gln Ile Ala Gly Ile  
 1490 1495

cct act gcc ttg agt gag tta ttt aaa aat gct cat gat gcc tat gct 4955  
 Pro Thr Ala Leu Ser Glu Leu Phe Lys Asn Ala His Asp Ala Tyr Ala  
 1500 1505 1510

gat aat gtc gaa gtt gat ttt ttt agg aaa gaa aat ctt ctt atc ttg 5003  
 Asp Asn Val Glu Val Asp Phe Phe Arg Lys Glu Asn Leu Leu Ile Leu  
 1515 1520 1525 1530

aga gat gat gga tta ggt atg aca acc gat gaa ttt gaa gag agg tgg 5051  
 Arg Asp Asp Gly Leu Gly Met Thr Thr Asp Glu Phe Glu Glu Arg Trp  
 1535 1540 1545

ttg act att gga acc tcc agc aaa tta atc gac gat gat gca att aat 5099  
 Leu Thr Ile Gly Thr Ser Ser Lys Leu Ile Asp Asp Asp Ala Ile Asn  
 1550 1555 1560

aaa cca gca gtg gat agt aat aaa gcc ttt cgc cct atc atg gga gag 5147  
 Lys Pro Ala Val Asp Ser Asn Lys Ala Phe Arg Pro Ile Met Gly Glu  
 1565 1570 1575

aaa gga ata ggc cgt tta tct atc gca gca att gga cca cag gtg ctg	5195
Lys Gly Ile Gly Arg Leu Ser Ile Ala Ala Ile Gly Pro Gln Val Leu	
1580 1585 1590	
ggt ctt act agg gcc aaa aga gac aat gag ctt aag cca tta gtt gct	5243
Val Leu Thr Arg Ala Lys Arg Asp Asn Glu Leu Lys Pro Leu Val Ala	
1595 1600 1605 1610	
gca ttt gtt aat tgg agt tta ttt gct ata cca tca ctt gat ctt gat	5291
Ala Phe Val Asn Trp Ser Leu Phe Ala Ile Pro Ser Leu Asp Leu Asp	
1615 1620 1625	
gat ata gaa ata cca att aga act att atc aac gac gaa tgc ttc act	5339
Asp Ile Glu Ile Pro Ile Arg Thr Ile Ile Asn Asp Glu Cys Phe Thr	
1630 1635 1640	
aaa aaa act ctt gat gag atg att gag caa gca aga aat aat tta gac	5387
Lys Lys Thr Leu Asp Glu Met Ile Glu Gln Ala Arg Asn Asn Leu Asp	
1645 1650 1655	
tct tta tca cac aaa ata tca aaa tca aaa gta tca caa ata aat aca	5435
Ser Leu Ser His Lys Ile Ser Lys Ser Lys Val Ser Gln Ile Asn Thr	
1660 1665 1670	
caa tta tca tct ttt gaa ttt gat cct att cta tgg gaa aaa aaa tta	5483
Gln Leu Ser Ser Phe Glu Phe Asp Pro Ile Leu Trp Glu Lys Lys Leu	
1675 1680 1685 1690	
ggg ggg cta aga cta tct gga gat ggg cat gga act cac ttc ata ata	5531
Gly Gly Leu Arg Leu Ser Gly Asp Gly His Gly Thr His Phe Ile Ile	
1695 1700 1705	
atg cct acc gaa gaa ata tta ata gat gac att tcc acg agc gat agc	5579
Met Pro Thr Glu Glu Ile Leu Ile Asp Asp Ile Ser Thr Ser Asp Ser	
1710 1715 1720	
aat aaa aca tca gag cag tct tct cgc tta gaa aaa gct tta tta ggt	5627
Asn Lys Thr Ser Glu Gln Ser Ser Arg Leu Glu Lys Ala Leu Leu Gly	
1725 1730 1735	
ttt aca aac aca atg tac agt gat tca aac cct cct att ata gct cgt	5675
Phe Thr Asn Thr Met Tyr Ser Asp Ser Asn Pro Pro Ile Ile Ala Arg	
1740 1745 1750	
ttt aga gac tat ctg gaa gat ggt gag tgc att gac aga att agc gaa	5723
Phe Arg Asp Tyr Leu Glu Asp Gly Glu Cys Ile Asp Arg Ile Ser Glu	
1755 1760 1765 1770	
tca att ttt ttt aca ccg caa gaa ttc aat ctt gca gat cac cac att	5771
Ser Ile Phe Phe Thr Pro Gln Glu Phe Asn Leu Ala Asp His His Ile	
1775 1780 1785	

gaa gga tgg ttc aat gaa ttt ggt caa ttc agt gga act gtt tct gtt Glu Gly Trp Phe Asn Glu Phe Gly Gln Phe Ser Gly Thr Val Ser Val 1790 1795 1800	5819
tat ggt gaa gag cca att cat cat gtc gtg act tgg aaa aat aat aat Tyr Gly Glu Glu Pro Ile His His Val Val Thr Trp Lys Asn Asn Asn 1805 1810 1815	5867
caa tta acc caa tgc ggt cca ttt aaa ata aaa tta gcg tat att cat Gln Leu Thr Gln Cys Gly Pro Phe Lys Ile Lys Leu Ala Tyr Ile His 1820 1825 1830	5915
ggt cgg ctt cgt gat tca cgc tta ccc atg gag ttg tgg gcc cct ctg Gly Arg Leu Arg Asp Ser Arg Leu Pro Met Glu Leu Trp Ala Pro Leu 1835 1840 1845 1850	5963
aag gag aaa aca gat aga tat ggt ggt tta tat atc tat cga gat gga Lys Glu Lys Thr Asp Arg Tyr Gly Gly Leu Tyr Ile Tyr Arg Asp Gly 1855 1860 1865	6011
tta aga att ttg ccc tat gga gat tca gat acg gat ttt cta aaa ata Leu Arg Ile Leu Pro Tyr Gly Asp Ser Asp Thr Asp Phe Leu Lys Ile 1870 1875 1880	6059
gaa aag aga aga acg tta tcc gct tct gaa tat ttt ttc tca tat cga Glu Lys Arg Arg Thr Leu Ser Ala Ser Glu Tyr Phe Phe Ser Tyr Arg 1885 1890 1895	6107
cgt ttg ttt gga gca ata gaa tta aca aaa gaa aac aat gct tca tta Arg Leu Phe Gly Ala Ile Glu Leu Thr Lys Glu Asn Asn Ala Ser Leu 1900 1905 1910	6155
gtt gaa aaa gct ggg cga gaa gga ttc att gaa aat aag cca tat aaa Val Glu Lys Ala Gly Arg Glu Gly Phe Ile Glu Asn Lys Pro Tyr Lys 1915 1920 1925 1930	6203
cag ttt aaa gaa atg ctt gaa aat ttc ttc atc gaa atc gca aga gat Gln Phe Lys Glu Met Leu Glu Asn Phe Phe Ile Glu Ile Ala Arg Asp 1935 1940 1945	6251
ttc ttt aag gac gat ggc gat atg tct gaa tta ttt gtt gag aca aag Phe Phe Lys Asp Asp Gly Asp Met Ser Glu Leu Phe Val Glu Thr Lys 1950 1955 1960	6299
caa cgt aga aat gaa gaa cat gat ttg tta tct aaa aga tct aaa caa Gln Arg Arg Asn Glu Glu His Asp Leu Leu Ser Lys Arg Ser Lys Gln 1965 1970 1975	6347
act aaa gct aaa aaa gat aga tta aag aaa gat ctg tat gat ttt ttt Thr Lys Ala Lys Lys Asp Arg Leu Lys Lys Asp Leu Tyr Asp Phe Phe 1980 1985 1990	6395

G:\SH-APPS\Seq\gje-65.Lx1\DNB\srp

acc gac cag att gca ata att agt gat agt acc act tct gaa aat tta	7067
Thr Asp Gln Ile Ala Ile Ile Ser Asp Ser Thr Thr Ser Glu Asn Leu	
2205 2210 2215	
tca tcg gct caa gta act gaa gca atc gaa act gaa ctt gaa cat tta	7115
Ser Ser Ala Gln Val Thr Glu Ala Ile Glu Thr Glu Leu Glu His Leu	
2220 2225 2230	
cga gac caa caa gca aat aac gca gag tta ata cta ctt ggc atg gct	7163
Arg Asp Gln Gln Ala Asn Asn Ala Glu Leu Ile Leu Leu Gly Met Ala	
2235 2240 2245 2250	
ctt tct gta gta cat cat gaa ttt aat ggt aat att agg gca att aga	7211
Leu Ser Val Val His His Glu Phe Asn Gly Asn Ile Arg Ala Ile Arg	
2255 2260 2265	
agt gcg cta agg gaa tta aaa gca tgg gct gac aga aat cct aag ctt	7259
Ser Ala Leu Arg Glu Leu Lys Ala Trp Ala Asp Arg Asn Pro Lys Leu	
2270 2275 2280	
gat att ata tac caa aaa atc aga act agt ttt gat cac tta gat ggt	7307
Asp Ile Ile Tyr Gln Lys Ile Arg Thr Ser Phe Asp His Leu Asp Gly	
2285 2290 2295	
tat tta aaa acc ttt aca cca ttg aca aga cgt tta agt cgc tct aaa	7355
Tyr Leu Lys Thr Phe Thr Pro Leu Thr Arg Arg Leu Ser Arg Ser Lys	
2300 2305 2310	
acc aat ata act gga act gcc att tta gaa ttt atc aga gat gta ttc	7403
Thr Asn Ile Thr Gly Thr Ala Ile Leu Glu Phe Ile Arg Asp Val Phe	
2315 2320 2325 2330	
gat gat cgt ctt gag aaa gaa gga att gaa tta ttc act acc tca aag	7451
Asp Asp Arg Leu Glu Lys Glu Gly Ile Glu Leu Phe Thr Thr Ser Lys	
2335 2340 2345	
ttt gtt aat caa gaa att gta act tac aca tca acc att tac cct gtc	7499
Phe Val Asn Gln Glu Ile Val Thr Tyr Thr Ser Thr Ile Tyr Pro Val	
2350 2355 2360	
ttt ata aat cta att gat aac gca ata tac tgg ctt ggg aaa aca act	7547
Phe Ile Asn Leu Ile Asp Asn Ala Ile Tyr Trp Leu Gly Lys Thr Thr	
2365 2370 2375	
gga gaa aaa aga ctt ata ctt gat gct act gaa aca gga ttt gtt att	7595
Gly Glu Lys Arg Leu Ile Leu Asp Ala Thr Glu Thr Gly Phe Val Ile	
2380 2385 2390	
ggg gat act ggt ccc ggt gtt tca act aga gat cga gat ata ata ttt	7643
Gly Asp Thr Gly Pro Gly Val Ser Thr Arg Asp Arg Asp Ile Ile Phe	
2395 2400 2405 2410	

gat atg gga ttt aca cga aaa aca gga ggg cgt gga atg gga tta ttc Asp Met Gly Phe Thr Arg Lys Thr Gly Gly Arg Gly Met Gly Leu Phe 2415 2420 2425	7691
att tcc aaa gag tgt tta tct cga gat gga ttt act ata aga ttg gat Ile Ser Lys Glu Cys Leu Ser Arg Asp Gly Phe Thr Ile Arg Leu Asp 2430 2435 2440	7739
gat tac act cct gaa cag ggt gct ttc ttt att att gag cca tca gaa Asp Tyr Thr Pro Glu Gln Gly Ala Phe Phe Ile Ile Glu Pro Ser Glu 2445 2450 2455	7787
gaa aca agt gaa tag cggatataaa taa atg aca agc tct act gat ttt Glu Thr Ser Glu Met Thr Ser Ser Thr Asp Phe 2460 2465 2470	7836
cat aaa ctt tct gaa gac tgc gtt cgc cgt ttt tta cat tct gta gtt His Lys Leu Ser Glu Asp Cys Val Arg Arg Phe Leu His Ser Val Val 2475 2480 2485	7884
gct gta gat gac aat atg tct ttt gga gct ggt agt gat act ttc cct Ala Val Asp Asp Asn Met Ser Phe Gly Ala Gly Ser Asp Thr Phe Pro 2490 2495 2500	7932
aca gac gaa gat att aat gct tta gtt gat ccc gac gat gat cct aca Thr Asp Glu Asp Ile Asn Ala Leu Val Asp Pro Asp Asp Asp Pro Thr 2505 2510 2515	7980
cca ata ata aca gca tca gca tcc cca agg ata gaa tca act aaa tca Pro Ile Ile Thr Ala Ser Ala Ser Pro Arg Ile Glu Ser Thr Lys Ser 2520 2525 2530	8028
aaa gca aag gta aaa aac cat cct ttt gat tac caa gct cta gca gaa Lys Ala Lys Val Lys Asn His Pro Phe Asp Tyr Gln Ala Leu Ala Glu 2535 2540 2545 2550	8076
gct ttc gcc aaa gat ggt att gct tgt tgc gga tta tta gct aag agt Ala Phe Ala Lys Asp Gly Ile Ala Cys Cys Gly Leu Leu Ala Lys Ser 2555 2560 2565	8124
ttt aat gtt gaa gaa aga gat ata att aca gca tca tcc cac aag gca Phe Asn Val Glu Glu Arg Asp Ile Ile Thr Ala Ser Ser His Lys Ala 2570 2575 2580	8172
gat ata aca ata ctt gac tgg gat atg caa agc gat agt ggg caa ttt Asp Ile Thr Ile Leu Asp Trp Asp Met Gln Ser Asp Ser Gly Gln Phe 2585 2590 2595	8220
gct att gaa ata ata aaa tcg ata atc gtt tca gat ata aat tct gga Ala Ile Glu Ile Ile Lys Ser Ile Ile Val Ser Asp Ile Asn Ser Gly 2600 2605 2610	8268



G:\SH-APPS\Seq\gje-65.tx\DNB\srp

att gaa cac gca tct tta ggt aaa aag gaa tac tta agc caa gat ggt Ile Glu His Ala Ser Leu Gly Lys Lys Glu Tyr Leu Ser Gln Asp Gly 2825 2830 2835	8940
gaa gaa gat aaa aag tta atg caa tta tgc tct ctg gaa atc acg cgc Glu Glu Asp Lys Lys Leu Met Gln Leu Cys Ser Leu Glu Ile Thr Arg 2840 2845 2850	8988
agg agt tta aga tat cat tct cat ata gat aat gtg tcc tta aaa caa Arg Ser Leu Arg Tyr His Ser His Ile Asp Asn Val Ser Leu Lys Gln 2855 2860 2865 2870	9036
gga act tta ctt tta gat gca tat aat ttt gtc tat cta tgc ata caa Gly Thr Leu Leu Leu Asp Ala Tyr Asn Phe Val Tyr Leu Cys Ile Gln 2875 2880 2885	9084
cca tta tgt gat agc gtc aga ttg cat gaa aaa gcc gat ttt tta ttc Pro Leu Cys Asp Ser Val Arg Leu His Glu Lys Ala Asp Phe Leu Phe 2890 2895 2900	9132
ctc agg gga aca ctg gac gat aat aat tac aat ttg tta atc gaa gat Leu Arg Gly Thr Leu Asp Asp Asn Asn Tyr Asn Leu Leu Ile Glu Asp 2905 2910 2915	9180
gaa tat ggc ggt ttt tat aaa att aaa atg ccg gca aaa gct tct aat Glu Tyr Gly Gly Phe Tyr Lys Ile Lys Met Pro Ala Lys Ala Ser Asn 2920 2925 2930	9228
att att tca ttt tca ttt gga gtc gaa aat gga aac ggt gtc atc ata Ile Ile Ser Phe Ser Phe Gly Val Glu Asn Gly Asn Gly Val Ile Ile 2935 2940 2945 2950	9276
ggg aaa aag aac aat cta gtt aat act gac tat atc tca ttc gtt cct Gly Lys Lys Asn Asn Leu Val Asn Thr Asp Tyr Ile Ser Phe Val Pro 2955 2960 2965	9324
tta ctc gtt gaa aaa ata tct act cca aaa gta ttg aaa tgg atc ggg Leu Leu Val Glu Lys Ile Ser Thr Pro Lys Val Leu Lys Trp Ile Gly 2970 2975 2980	9372
gaa ata aaa aca acg tac gcg caa aaa ata aca act gat att gtt gct Glu Ile Lys Thr Thr Tyr Ala Gln Lys Ile Thr Thr Asp Ile Val Ala 2985 2990 2995	9420
aat ctg tca aga ata ggt tta gat caa cat gag tgg tta cga ata aaa Asn Leu Ser Arg Ile Gly Leu Asp Gln His Glu Trp Leu Arg Ile Lys 3000 3005 3010	9468
tca aaa gat ata taaatgatta tatatgccgt cggtttataa aaactggcgg Ser Lys Asp Ile 3015	9520

catgtatatc tagttagtcc atcatagaag tcaagaaatt tagtttgccc tatatcttat 9580  
agaaaaatata ttttatatgc ttaaaaaaca ccatctttct aagatggcat ttatgtgctt 9640  
tgtttcgatac aattacaact gatataattac catattgatt aattttatgt tatttaccaa 9700  
agtaacggca tcttaatata tcgtcataat atagtgcgcg ttctgactct aatactgaaa 9760  
aatttatttg ttctatttta cacttactgc aaatagcatc cagtttatca tatagtgtcg 9820  
catcaattgg cgcag atg tca tca cgc caa atc ctt gag cat tat aat gct 9871  
Met Ser Ser Arg Gln Ile Leu Glu His Tyr Asn Ala  
3020 3025 3030  
cta aca tat ccc cta cat caa tca atc ttg ttg cag ata atg act tcg 9919  
Leu Thr Tyr Pro Leu His Gln Ser Ile Leu Leu Gln Ile Met Thr Ser  
3035 3040 3045  
aat ttg tta tca gtt tgc act gga aaa tcc att tac gag gat atc tcc 9967  
Asn Leu Leu Ser Val Cys Thr Gly Lys Ser Ile Tyr Glu Asp Ile Ser  
3050 3055 3060  
ggc agt tct tgg aat atc ata cac ttc aat atc cct ctg ccc atc tct 10015  
Gly Ser Ser Trp Asn Ile Ile His Phe Asn Ile Pro Leu Pro Ile Ser  
3065 3070 3075  
aga gcg aga ctt tcc ata ttt tct tat tgt gtc aga att aaa cct tgg 10063  
Arg Ala Arg Leu Ser Ile Phe Ser Tyr Cys Val Arg Ile Lys Pro Trp  
3080 3085 3090  
atg agt atg gat tac atg taaccggctc atttaaaccg tctggtctgt 10111  
Met Ser Met Asp Tyr Met  
3095 3100  
ttcctccggt tttaaaaaa ta atg tcc atc att ttt aat gga cac tat cgt 10163  
Met Ser Ile Ile Phe Asn Gly His Tyr Arg  
3105 3110  
atg aaa cac cgg act tgg atc act gaa gct tta cgt ctt cac ttt gaa 10211  
Met Lys His Arg Thr Trp Ile Thr Glu Ala Leu Arg Leu His Phe Glu  
3115 3120 3125  
gaa cat tta ccc cag gtt gtg gtc ggg cgt cgc ctg ggc gta cca aaa 10259  
Glu His Leu Pro Gln Val Val Val Gly Arg Arg Leu Gly Val Pro Lys  
3130 3135 3140  
tca aca gct tgt ggt atg ttc gtg cgc ttt cgc aaa gct ggc ttt tca 10307  
Ser Thr Ala Cys Gly Met Phe Val Arg Phe Arg Lys Ala Gly Phe Ser  
3145 3150 3155  
tgg cct ctg ccc gca ggt atg tcg gag cgg gag ctt gat ggc cgt ctt 10355

Trp Pro Leu Pro Ala Gly Met Ser Glu Arg Glu Leu Asp Gly Arg Leu  
 3160 3165 3170  
 tac ggg agt acc tcc aca gta cct gtc gta ctt tgt agt gga tcg gta 10403  
 Tyr Gly Ser Thr Ser Thr Val Pro Val Val Leu Cys Ser Gly Ser Val  
 3175 3180 3185 3190  
 att cag gac acc tcg aaa tcc tgt taatgttaaa acagtgaataa tgagggtgatg 10457  
 Ile Gln Asp Thr Ser Lys Ser Cys  
 3195  
 c atg atc aaa act cgt cgg act aaa cgt acc ttt tcc ccg gag ttc aag 10506  
 Met Ile Lys Thr Arg Arg Thr Lys Arg Thr Phe Ser Pro Glu Phe Lys  
 3200 3205 3210  
 ctt gaa gct ttc gag cag gtg gtg gtt aaa tac cag cgt gat gtc aga 10554  
 Leu Glu Ala Phe Glu Gln Val Val Val Lys Tyr Gln Arg Asp Val Arg  
 3215 3220 3225 3230  
 gaa gtc gcg cag gca ctc gag ctc aac cct gac cat ttg cgt aaa tgg 10602  
 Glu Val Ala Gln Ala Leu Glu Leu Asn Pro Asp His Leu Arg Lys Trp  
 3235 3240 3245  
 ata cgg ttg tat aag cag gaa ctt cag ggt att gag cca gct ggt aat 10650  
 Ile Arg Leu Tyr Lys Gln Glu Leu Gln Gly Ile Glu Pro Ala Gly Asn  
 3250 3255 3260  
 gct att acc cct gaa caa cgc gaa att cag cag ctt aaa gcg cag ata 10698  
 Ala Ile Thr Pro Glu Gln Arg Glu Ile Gln Gln Leu Lys Ala Gln Ile  
 3265 3270 3275  
 aag cgc gtt gag atg gaa aaa gaa ata cta aag cag gct gcc gtg ctg 10746  
 Lys Arg Val Glu Met Glu Lys Glu Ile Leu Lys Gln Ala Ala Val Leu  
 3280 3285 3290  
 atg agc gaa atc ccc ggg aag ctg tcg cgc taatcacaca gctgaaagca 10796  
 Met Ser Glu Ile Pro Gly Lys Leu Ser Arg  
 3295 3300  
 aagtggccag tgtgggttat ttgtcattta ttcggtatta accgtagcgt ttattacgcg 10856  
 caggtgaagc gtctgtttaa tgtgcaaaga attgaattac gaagccgggt gagggctttc 10916  
 catgctctca gtcgtggcgc agccgggtag ccgggcaatc agtcagatgt tgcgccagag 10976  
 tggcgttgat gcagggcgggt ggctggcatg acgactgatg cgggaatgag ggctgacaag 11036  
 tcgacagccg gttaaaccatc acaaccgggt aaacgaagac aaaagtccgc cattgccaaa 11096  
 ttactgaac cggcaatttc accccgccgc accaaactgc gtctgggtgcg gcgacatcag 11156

ttttattcg

11165

&lt;210&gt; 35

&lt;211&gt; 366

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 35

Ser Asp Met Gln Arg Gly Ile Gln Ala Ala Thr Ala Ala Leu Gln Gly  
 1 5 10 15

Leu Val Gly Gly Asn Met Ala Gly Ala Leu Ala Gly Ala Ser Ala Pro  
 20 25 30

Glu Leu Ala Asn Ile Ile Gly His His Ala Gly Ile Asp Asp Asn Thr  
 35 40 45

Ala Ala Lys Ala Ile Ala His Ala Ile Leu Gly Gly Val Thr Ala Ala  
 50 55 60

Leu Gln Gly Asn Ser Ala Ala Ala Gly Ala Ile Gly Ala Gly Thr Gly  
 65 70 75 80

Glu Val Ile Ala Ser Ala Ile Ala Lys Ser Leu Tyr Pro Gly Val Asp  
 85 90 95

Pro Ser Lys Leu Thr Glu Asp Gln Lys Gln Thr Val Ser Thr Leu Ala  
 100 105 110

Thr Leu Ser Ala Gly Met Ala Gly Gly Ile Ala Ser Gly Asp Val Ala  
 115 120 125

Gly Ala Ala Ala Gly Ala Gly Ala Gly Lys Asn Val Val Glu Asn Asn  
 130 135 140

Ala Leu Ser Leu Val Ala Arg Gly Cys Ala Val Ala Ala Pro Cys Arg  
 145 150 155 160

Thr Lys Val Ala Glu Gln Leu Leu Glu Ile Gly Ala Lys Ala Gly Met  
 165 170 175

Ala Gly Leu Ala Gly Ala Ala Val Lys Asp Met Ala Asp Arg Met Thr  
 180 185 190

Ser Asp Glu Leu Glu His Leu Ile Thr Leu Gln Met Met Gly Asn Asp  
 195 200 205

Glu Ile Thr Thr Lys Tyr Leu Ser Ser Leu His Asp Lys Tyr Gly Ser  
 210 215 220

Gly Ala Ala Ser Asn Pro Asn Ile Gly Lys Asp Leu Thr Asp Ala Glu  
 225 230 235 240  
 Lys Val Glu Leu Gly Gly Ser Gly Ser Gly Thr Gly Thr Pro Pro Pro  
 245 250 255  
 Ser Glu Asn Asp Pro Lys Gln Gln Asn Glu Lys Thr Val Asp Lys Leu  
 260 265 270  
 Asn Gln Lys Gln Glu Ser Ala Ile Lys Lys Ile Asp Asn Thr Ile Lys  
 275 280 285  
 Asn Ala Leu Lys Asp His Asp Ile Ile Gly Thr Leu Lys Asp Met Asp  
 290 295 300  
 Gly Lys Pro Val Pro Lys Glu Asn Gly Gly Tyr Trp Asp His Met Gln  
 305 310 315 320  
 Glu Met Gln Asn Thr Leu Arg Gly Leu Arg Asn His Ala Asp Thr Leu  
 325 330 335  
 Lys Asn Val Asn Asn Pro Glu Ala Gln Ala Ala Tyr Gly Arg Ala Thr  
 340 345 350  
 Asp Ala Ile Asn Lys Ile Glu Ser Ala Leu Lys Gly Tyr Gly  
 355 360 365

<210> 36  
 <211> 128  
 <212> PRT  
 <213> Escherichia coli

<400> 36  
 Met Ile Thr Leu Arg Lys Leu Ile Gly Asn Ile Asn Met Thr Lys Glu  
 1 5 10 15  
 Pro Glu Gln Gln Ser Pro Leu Glu Leu Trp Phe Glu Arg Ile Ile Asp  
 20 25 30  
 Val Pro Leu Glu Lys Leu Thr Val Glu Asp Leu Cys Arg Ala Ile Arg  
 35 40 45  
 Gln Asn Leu Cys Ile Asp Gln Leu Met Pro Arg Val Leu Glu Val Leu  
 50 55 60  
 Thr Lys Glu Pro Leu Ala Gly Glu Tyr Tyr Asp Gly Glu Leu Ile Ala  
 65 70 75 80  
 Ala Leu Ser Thr Ile Lys Gly Glu Asp Leu Lys Asp Gln Lys Ser Thr  
 85 90 95

Phe Thr Gln Ile Arg Gln Leu Ile Asn Gln Leu Glu Pro Ser Asp Ile  
 100 105 110

Asn Asp Asp Leu Arg Lys Asp Ile Leu Lys Ile Asn Gln Ile Ile Val  
 115 120 125

<210> 37

<211> 107

<212> PRT

<213> Escherichia coli

<400> 37

Met Val Ala Lys Ala Phe Ala Tyr Ala Leu Asn Gln Trp Pro Ala Leu  
 1 5 10 15

Thr Tyr Tyr Ala Asn Asp Gly Trp Val Glu Ile Asp Asn Asn Ile Ala  
 20 25 30

Glu Asn Ala Leu Arg Ala Val Ser Leu Gly Arg Lys Asn Phe Leu Phe  
 35 40 45

Phe Gly Ser Asp His Gly Gly Glu Arg Gly Ala Leu Leu Tyr Ser Leu  
 50 55 60

Ile Gly Thr Cys Lys Leu Asn Asp Val Asp Pro Glu Ser Tyr Leu Arg  
 65 70 75 80

His Val Leu Ala Val Ile Ala Asp Trp Pro Val Asn Arg Val Ser Glu  
 85 90 95

Leu Leu Pro Trp Arg Ile Ala Leu Pro Ala Glu  
 100 105

<210> 38

<211> 86

<212> PRT

<213> Escherichia coli

<400> 38

Met Leu Met Ser Val Gln Lys Glu Lys Asn Val Ala Glu Ser Val Val  
 1 5 10 15

Ser Glu Thr His Thr Gly Asp Ser Val Tyr Ala Ser Leu Phe Glu Lys  
 20 25 30

Ile Asn Leu Asn Pro Val Ser Ala Leu Ser Ala Leu Asp Asn Pro Phe  
 35 40 45

Arg Ser Ala Asp Asn Ala Thr Gly Arg Ile Thr Ser Ser Ile Gln Pro

50                      55                      60

Ala Val Gln Cys Ala Ala Ala Ala Ala Thr Glu Gly Ser Cys Pro Arg  
 65                      70                      75                      80

Gln Ser Pro Cys Ser Gly  
                                  85

<210> 39  
 <211> 111  
 <212> PRT  
 <213> Escherichia coli

<400> 39

Met Val Asp Asn Trp Gln Lys Ser Val Arg Ser Arg Ala Leu Pro Glu  
 1                      5                      10                      15

Glu Ala Met Thr Gly Trp Asn Glu Gly Met Ile Arg Leu Gln Gln Leu  
                                  20                      25                      30

Ala Glu Arg Leu Asn Arg Gln Asp Glu Gln Arg Gly Lys Tyr Met Thr  
                                  35                      40                      45

Val Ser Glu Leu Lys Thr Glu Val Phe Gly Ile Met Gln Ala Phe Asn  
                                  50                      55                      60

Arg His Ile Pro Ala Glu Glu Gln Leu Arg Arg Tyr Gly Glu Val Arg  
 65                      70                      75                      80

Asn Gln Asn Gly Ser Glu Gln Gln Gln Lys Gln Ala Glu Met Ala Leu  
                                  85                      90                      95

Asn Gln Leu Ile Asn Arg Tyr Gln Met Ile Arg Ala Gly Lys Gln  
                                  100                      105                      110

<210> 40  
 <211> 143  
 <212> PRT  
 <213> Escherichia coli

<400> 40

Met Val Gly Cys Ala Trp Leu Ala Glu Gln Ala Phe Ser Asp His Ala  
 1                      5                      10                      15

Leu Ser Pro His Ser Ala Trp Pro Tyr Ser Ala Ser Arg Asp Ala Gly  
                                  20                      25                      30

Leu Ala Asp Thr Gly Ala Gly Gly Tyr Pro Thr Cys Lys Gln Arg Trp  
                                  35                      40                      45



Ala Asp Asp Thr Val Gly Leu Lys Ala Arg Leu Leu Gln Leu Pro Ala  
 50 55 60

Leu Asp Ile Trp Thr Ala Phe Lys Lys Ile Asp Gln Ser Gln Val Val  
 65 70 75 80

Tyr Glu Glu Ala Val Leu Arg Ser Arg Val Ser Glu Arg Asn Met Gln  
 85 90 95

Val Ser Gln Asn Gly Arg Val Tyr Pro Ser Tyr Gly Gly Asn Val Asp  
 100 105 110

Gly Thr Val Ala Asn Ala Ala Thr Arg Leu Ala Ser Gly Ala Arg Asn  
 115 120 125

Ile Leu Gly Ser Ile Ala Ala Cys Thr Ala Phe Asp Ser Val Arg  
 130 135 140

<210> 41

<211> 118

<212> PRT

<213> Escherichia coli

<400> 41

Met Val Gln Ala Gln Leu Gln Ile Ala Leu Val Ile Cys Ile Pro Leu  
 1 5 10 15

Ile Thr Leu Cys Ser Ala Trp Asp Val Lys Val Val Met Thr Leu Thr  
 20 25 30

Phe Val Gln Phe Ala Leu Phe Phe Leu Thr Phe Trp Trp Glu Leu Ala  
 35 40 45

Arg Trp Leu Asp Ser Trp Leu Leu Asp Val Leu Tyr Asn Ser Asp Thr  
 50 55 60

His Ser Ser Trp Asn Leu Ala Gly Ile Gln Asn Thr Gln Asp Asp Val  
 65 70 75 80

Ile Ile Asn Leu Val Met Arg Leu Met Phe Leu Val Leu Pro Thr Phe  
 85 90 95

Trp Leu Gly Ala Met Thr Trp Ala Gly Val Arg Val Gly Val Ala Leu  
 100 105 110

Asn Gly Ala Leu Ala Gly  
 115

<210> 42

<211> 81  
 <212> PRT  
 <213> Escherichia coli

<400> 42  
 Met Lys Tyr Leu Phe Phe Glu Asn Ile His Ser Ile Phe Leu Thr Phe  
     1                    5                    10                    15  
 Ser Leu Phe Arg Thr Ser Val Ser Pro Asp Phe Pro Met Ile Phe Ala  
                     20                    25                    30  
 Leu Pro Ser Ile Ile Leu Gly Gln Phe Thr Thr Asn Gln Leu Thr Asn  
                     35                    40                    45  
 Phe Val Ile Cys Met Gly Asn Thr Val Glu Arg Arg Leu Gly Val Val  
                     50                    55                    60  
 His Asn Pro Phe Lys Arg Ser Gly Asp Gly His Asp Leu Arg Ala Val  
     65                    70                    75                    80  
 Ala

<210> 43  
 <211> 348  
 <212> PRT  
 <213> Escherichia coli

<400> 43  
 Leu Ile Val Ile Asp Phe Phe Cys Gly Cys Gly Gly Ala Ser Glu Gly  
     1                    5                    10                    15  
 Leu Arg Gln Ala Gly Phe Asp Ile Glu Leu Gly Leu Asp Ile Asp Gln  
                     20                    25                    30  
 Gln Ala Ser Glu Thr Phe Lys Ala Asn Phe Pro Asp Ala Lys Phe Ile  
                     35                    40                    45  
 Gln Asp Asp Ile Arg Lys Ile Glu Pro Gln Asp Ile Ser Asp Ile Ile  
                     50                    55                    60  
 Asp Ile Lys Ala Lys Arg Pro Leu Leu Leu Ser Ala Cys Ala Pro Cys  
     65                    70                    75                    80  
 Gln Pro Phe Ser Gln Gln Asn Lys Asn Lys Thr Ser Asp Asp Ser Arg  
                     85                    90                    95  
 Arg Asn Leu Leu Asn Glu Thr His Arg Phe Ile Arg Glu Leu Leu Pro  
                     100                    105                    110  
 Glu Tyr Ile Met Leu Glu Asn Val Pro Gly Met Gln Lys Ile Asp Glu

115	120	125
Glu Lys Glu Gly Pro Phe Gln Glu Phe Ile Lys Leu Leu Lys Glu Leu		
130	135	140
Glu Tyr Asn Tyr Ile Ser Phe Ile Ala Asn Ala Glu Asn Tyr Gly Ile		
145	150	155 160
Pro Gln Arg Arg Lys Arg Leu Val Leu Leu Ala Ser Arg Val Gly Lys		
	165	170 175
Val Thr Leu Pro Glu Ile Thr His Gly Lys Asn Lys Ile Pro Phe Lys		
	180	185 190
Thr Val Arg Asp Tyr Ile Gln Asp Phe Thr Lys Leu Cys Ser Gly Glu		
	195	200 205
Thr Asp Pro Lys Asp Pro Leu His Arg Ala Gly Thr Leu Ser Pro Leu		
	210	215 220
Asn Leu Lys Arg Ile Met His Thr Pro Glu Gly Gly Asp Arg Arg Asn		
225	230	235 240
Trp Pro Glu Glu Leu Val Asn Lys Cys His Lys Asn Tyr Asp Gly His		
	245	250 255
Thr Asp Thr Tyr Gly Arg Met Ser Trp Asp Lys Pro Ala Pro Thr Leu		
	260	265 270
Thr Thr Lys Cys Asn Ser Tyr Ser Asn Gly Arg Phe Gly His Pro Asp		
	275	280 285
Pro Thr Gln His Arg Ala Ile Ser Ile Arg Glu Ala Ser Arg Leu Gln		
	290	295 300
Thr Phe Pro Leu Ser Tyr Val Phe Lys Gly Ser Leu Asn Ser Met Ala		
305	310	315 320
Lys Gln Ile Gly Asn Ala Val Pro Cys Glu Leu Ala Arg Leu Phe Gly		
	325	330 335
Leu His Leu Ile Glu Asn Cys Thr Asn Lys Asp Ser		
	340	345

&lt;210&gt; 44

&lt;211&gt; 974

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 44

Met Leu Gly Arg Gln Gln Ile Ala Gly Ile Pro Thr Ala Leu Ser Glu  
 1 5 10 15  
 Leu Phe Lys Asn Ala His Asp Ala Tyr Ala Asp Asn Val Glu Val Asp  
 20 25 30  
 Phe Phe Arg Lys Glu Asn Leu Leu Ile Leu Arg Asp Asp Gly Leu Gly  
 35 40 45  
 Met Thr Thr Asp Glu Phe Glu Glu Arg Trp Leu Thr Ile Gly Thr Ser  
 50 55 60  
 Ser Lys Leu Ile Asp Asp Asp Ala Ile Asn Lys Pro Ala Val Asp Ser  
 65 70 75 80  
 Asn Lys Ala Phe Arg Pro Ile Met Gly Glu Lys Gly Ile Gly Arg Leu  
 85 90 95  
 Ser Ile Ala Ala Ile Gly Pro Gln Val Leu Val Leu Thr Arg Ala Lys  
 100 105 110  
 Arg Asp Asn Glu Leu Lys Pro Leu Val Ala Ala Phe Val Asn Trp Ser  
 115 120 125  
 Leu Phe Ala Ile Pro Ser Leu Asp Leu Asp Asp Ile Glu Ile Pro Ile  
 130 135 140  
 Arg Thr Ile Ile Asn Asp Glu Cys Phe Thr Lys Lys Thr Leu Asp Glu  
 145 150 155 160  
 Met Ile Glu Gln Ala Arg Asn Asn Leu Asp Ser Leu Ser His Lys Ile  
 165 170 175  
 Ser Lys Ser Lys Val Ser Gln Ile Asn Thr Gln Leu Ser Ser Phe Glu  
 180 185 190  
 Phe Asp Pro Ile Leu Trp Glu Lys Lys Leu Gly Gly Leu Arg Leu Ser  
 195 200 205  
 Gly Asp Gly His Gly Thr His Phe Ile Ile Met Pro Thr Glu Glu Ile  
 210 215 220  
 Leu Ile Asp Asp Ile Ser Thr Ser Asp Ser Asn Lys Thr Ser Glu Gln  
 225 230 235 240  
 Ser Ser Arg Leu Glu Lys Ala Leu Leu Gly Phe Thr Asn Thr Met Tyr  
 245 250 255  
 Ser Asp Ser Asn Pro Pro Ile Ile Ala Arg Phe Arg Asp Tyr Leu Glu  
 260 265 270

Asp Gly Glu Cys Ile Asp Arg Ile Ser Glu Ser Ile Phe Phe Thr Pro  
 275 280 285  
 Gln Glu Phe Asn Leu Ala Asp His His Ile Glu Gly Trp Phe Asn Glu  
 290 295 300  
 Phe Gly Gln Phe Ser Gly Thr Val Ser Val Tyr Gly Glu Glu Pro Ile  
 305 310 315 320  
 His His Val Val Thr Trp Lys Asn Asn Asn Gln Leu Thr Gln Cys Gly  
 325 330 335  
 Pro Phe Lys Ile Lys Leu Ala Tyr Ile His Gly Arg Leu Arg Asp Ser  
 340 345 350  
 Arg Leu Pro Met Glu Leu Trp Ala Pro Leu Lys Glu Lys Thr Asp Arg  
 355 360 365  
 Tyr Gly Gly Leu Tyr Ile Tyr Arg Asp Gly Leu Arg Ile Leu Pro Tyr  
 370 375 380  
 Gly Asp Ser Asp Thr Asp Phe Leu Lys Ile Glu Lys Arg Arg Thr Leu  
 385 390 395 400  
 Ser Ala Ser Glu Tyr Phe Phe Ser Tyr Arg Arg Leu Phe Gly Ala Ile  
 405 410 415  
 Glu Leu Thr Lys Glu Asn Asn Ala Ser Leu Val Glu Lys Ala Gly Arg  
 420 425 430  
 Glu Gly Phe Ile Glu Asn Lys Pro Tyr Lys Gln Phe Lys Glu Met Leu  
 435 440 445  
 Glu Asn Phe Phe Ile Glu Ile Ala Arg Asp Phe Phe Lys Asp Asp Gly  
 450 455 460  
 Asp Met Ser Glu Leu Phe Val Glu Thr Lys Gln Arg Arg Asn Glu Glu  
 465 470 475 480  
 His Asp Leu Leu Ser Lys Arg Ser Lys Gln Thr Lys Ala Lys Lys Asp  
 485 490 495  
 Arg Leu Lys Lys Asp Leu Tyr Asp Phe Phe Asp Lys Leu Asp Asn Asp  
 500 505 510  
 Tyr Trp Asn Ile Glu Ile Asn Lys Leu Ile Asn Lys Asn Glu Glu Tyr  
 515 520 525  
 Phe Ser Ser Thr Glu Ile Thr Asp Thr Asn Ile Asp Tyr Val Tyr Asn  
 530 535 540

Lys Ile Lys Glu Gln Asn Asp Ala Ile Ile Lys Asn Leu Arg Asn Ser  
 545 550 555 560  
 Val Asp Ile Lys Lys Pro Ser Gly Val Gly Leu Thr Lys Glu Leu Ser  
 565 570 575  
 Asn Leu Trp Asp Arg Tyr Gln Ile Glu Arg Gln Lys Ile Leu Leu Ser  
 580 585 590  
 Leu Asn Glu Leu Lys Asp Asn Val Asp Arg Lys Leu Ile Glu Leu Asp  
 595 600 605  
 Asn Lys Asn Asn Asp Phe Leu Asn Leu Arg Lys Arg Leu Glu Asp Ser  
 610 615 620  
 Leu Asn Leu Gln Gln Ser Tyr Tyr Glu Lys Glu Leu Thr Lys Leu Tyr  
 625 630 635 640  
 Asn Asp Ala Lys Asn Ala Leu Lys Asp Val Gln Ser Lys Ala Asn Arg  
 645 650 655  
 Leu Ile Ser Asp Asn Lys Lys Lys His Lys Ser Glu Leu Lys Asn Ile  
 660 665 670  
 Ser Tyr Glu Phe Gln Ser Thr Asn Leu Asn Gly Lys Asp Thr Ala Tyr  
 675 680 685  
 Ile Leu Asp Val Lys Arg Asn Leu Glu Ser Lys Ile Glu Asn Thr Ser  
 690 695 700  
 Asn Glu Val Ile Asn Glu Ile Arg Lys Leu Thr Asp Gln Ile Ala Ile  
 705 710 715 720  
 Ile Ser Asp Ser Thr Thr Ser Glu Asn Leu Ser Ser Ala Gln Val Thr  
 725 730 735  
 Glu Ala Ile Glu Thr Glu Leu Glu His Leu Arg Asp Gln Gln Ala Asn  
 740 745 750  
 Asn Ala Glu Leu Ile Leu Leu Gly Met Ala Leu Ser Val Val His His  
 755 760 765  
 Glu Phe Asn Gly Asn Ile Arg Ala Ile Arg Ser Ala Leu Arg Glu Leu  
 770 775 780  
 Lys Ala Trp Ala Asp Arg Asn Pro Lys Leu Asp Ile Ile Tyr Gln Lys  
 785 790 795 800  
 Ile Arg Thr Ser Phe Asp His Leu Asp Gly Tyr Leu Lys Thr Phe Thr  
 805 810 815

Pro Leu Thr Arg Arg Leu Ser Arg Ser Lys Thr Asn Ile Thr Gly Thr  
                     820                    825                    830  
 Ala Ile Leu Glu Phe Ile Arg Asp Val Phe Asp Asp Arg Leu Glu Lys  
                     835                    840                    845  
 Glu Gly Ile Glu Leu Phe Thr Thr Ser Lys Phe Val Asn Gln Glu Ile  
                     850                    855                    860  
 Val Thr Tyr Thr Ser Thr Ile Tyr Pro Val Phe Ile Asn Leu Ile Asp  
                     865                    870                    875                    880  
 Asn Ala Ile Tyr Trp Leu Gly Lys Thr Thr Gly Glu Lys Arg Leu Ile  
                     885                    890                    895  
 Leu Asp Ala Thr Glu Thr Gly Phe Val Ile Gly Asp Thr Gly Pro Gly  
                     900                    905                    910  
 Val Ser Thr Arg Asp Arg Asp Ile Ile Phe Asp Met Gly Phe Thr Arg  
                     915                    920                    925  
 Lys Thr Gly Gly Arg Gly Met Gly Leu Phe Ile Ser Lys Glu Cys Leu  
                     930                    935                    940  
 Ser Arg Asp Gly Phe Thr Ile Arg Leu Asp Asp Tyr Thr Pro Glu Gln  
                     945                    950                    955                    960  
 Gly Ala Phe Phe Ile Ile Glu Pro Ser Glu Glu Thr Ser Glu  
                     965                    970

<210> 45

<211> 555

<212> PRT

<213> Escherichia coli

<400> 45

Met Thr Ser Ser Thr Asp Phe His Lys Leu Ser Glu Asp Cys Val Arg  
   1                    5                    10                    15  
 Arg Phe Leu His Ser Val Val Ala Val Asp Asp Asn Met Ser Phe Gly  
                     20                    25                    30  
 Ala Gly Ser Asp Thr Phe Pro Thr Asp Glu Asp Ile Asn Ala Leu Val  
                     35                    40                    45  
 Asp Pro Asp Asp Asp Pro Thr Pro Ile Ile Thr Ala Ser Ala Ser Pro  
                     50                    55                    60  
 Arg Ile Glu Ser Thr Lys Ser Lys Ala Lys Val Lys Asn His Pro Phe  
                     65                    70                    75                    80

Asp Tyr Gln Ala Leu Ala Glu Ala Phe Ala Lys Asp Gly Ile Ala Cys  
                     85                    90                    95  
 Cys Gly Leu Leu Ala Lys Ser Phe Asn Val Glu Glu Arg Asp Ile Ile  
                     100                    105                    110  
 Thr Ala Ser Ser His Lys Ala Asp Ile Thr Ile Leu Asp Trp Asp Met  
                     115                    120                    125  
 Gln Ser Asp Ser Gly Gln Phe Ala Ile Glu Ile Ile Lys Ser Ile Ile  
                     130                    135                    140  
 Val Ser Asp Ile Asn Ser Gly Gly Arg Leu Arg Leu Leu Ser Ile Tyr  
                     145                    150                    155                    160  
 Thr Gly Glu His Val Thr Ala Val Ile Thr Lys Leu Asn Asn Glu Leu  
                     165                    170                    175  
 Lys Lys Thr Tyr Arg Ser Val Ile Lys Asn Asp Asp Ser Ile Phe Ile  
                     180                    185                    190  
 Glu Asp Asn Tyr Ala Leu Glu Gln Trp Cys Ile Val Val Ile Ser Lys  
                     195                    200                    205  
 Asp Val Tyr Glu Lys Asp Leu Pro Asn Val Leu Ile Lys Lys Phe Thr  
                     210                    215                    220  
 Asn Leu Thr Ala Gly Leu Leu Ser Asn Ala Ala Leu Ser Cys Ile Ser  
                     225                    230                    235                    240  
 Glu Ile Arg Glu Lys Thr His Gly Ile Leu Thr Lys Tyr Asn Asn Lys  
                     245                    250                    255  
 Leu Asp Thr Ala Tyr Val Ser His Ile Leu Asn Leu Ile Lys Ser Lys  
                     260                    265                    270  
 Glu Ser Arg Ala Tyr Ala Tyr Glu Asn Ala His Asp Tyr Ala Val Asp  
                     275                    280                    285  
 Leu Ile Ser Glu Glu Ile Arg Ser Ile Leu Gln Ile Ser Glu Asn Leu  
                     290                    295                    300  
 Lys Lys Ser Leu Ser Lys Asn Ser Leu Ser His Trp Pro Ile Phe His  
                     305                    310                    315                    320  
 Tyr Ala Lys Asn Gly Cys Lys Asn Phe Leu Leu Thr Gly Lys Lys Gln  
                     325                    330                    335  
 Lys Asp Leu Ser Val Glu His Leu Arg Asn Ile Leu Ser Ala Asp Ser  
                     340                    345                    350



Leu Glu Glu Ile Gln His Ala Ile Glu His Ala Ser Leu Gly Lys Lys  
           355                          360                          365  
 Glu Tyr Leu Ser Gln Asp Gly Glu Glu Asp Lys Lys Leu Met Gln Leu  
           370                          375                          380  
 Cys Ser Leu Glu Ile Thr Arg Arg Ser Leu Arg Tyr His Ser His Ile  
   385                          390                          395                          400  
 Asp Asn Val Ser Leu Lys Gln Gly Thr Leu Leu Leu Asp Ala Tyr Asn  
                           405                          410                          415  
 Phe Val Tyr Leu Cys Ile Gln Pro Leu Cys Asp Ser Val Arg Leu His  
                           420                          425                          430  
 Glu Lys Ala Asp Phe Leu Phe Leu Arg Gly Thr Leu Asp Asp Asn Asn  
           435                          440                          445  
 Tyr Asn Leu Leu Ile Glu Asp Glu Tyr Gly Gly Phe Tyr Lys Ile Lys  
           450                          455                          460  
 Met Pro Ala Lys Ala Ser Asn Ile Ile Ser Phe Ser Phe Gly Val Glu  
   465                          470                          475                          480  
 Asn Gly Asn Gly Val Ile Ile Gly Lys Lys Asn Asn Leu Val Asn Thr  
                           485                          490                          495  
 Asp Tyr Ile Ser Phe Val Pro Leu Leu Val Glu Lys Ile Ser Thr Pro  
                           500                          505                          510  
 Lys Val Leu Lys Trp Ile Gly Glu Ile Lys Thr Thr Tyr Ala Gln Lys  
           515                          520                          525  
 Ile Thr Thr Asp Ile Val Ala Asn Leu Ser Arg Ile Gly Leu Asp Gln  
           530                          535                          540  
 His Glu Trp Leu Arg Ile Lys Ser Lys Asp Ile  
   545                          550                          555

&lt;210&gt; 46

&lt;211&gt; 82

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 46

Met Ser Ser Arg Gln Ile Leu Glu His Tyr Asn Ala Leu Thr Tyr Pro  
   1                          5                          10                          15

Leu His Gln Ser Ile Leu Leu Gln Ile Met Thr Ser Asn Leu Leu Ser  
           20                          25                          30

Val Cys Thr Gly Lys Ser Ile Tyr Glu Asp Ile Ser Gly Ser Ser Trp  
                   35                                  40                                  45

Asn Ile Ile His Phe Asn Ile Pro Leu Pro Ile Ser Arg Ala Arg Leu  
           50                                  55                                  60

Ser Ile Phe Ser Tyr Cys Val Arg Ile Lys Pro Trp Met Ser Met Asp  
       65                                  70                                  75                                  80

Tyr Met

<210> 47  
 <211> 98  
 <212> PRT  
 <213> Escherichia coli

<400> 47  
 Met Ser Ile Ile Phe Asn Gly His Tyr Arg Met Lys His Arg Thr Trp  
       1                                  5                                  10                                  15

Ile Thr Glu Ala Leu Arg Leu His Phe Glu Glu His Leu Pro Gln Val  
                   20                                  25                                  30

Val Val Gly Arg Arg Leu Gly Val Pro Lys Ser Thr Ala Cys Gly Met  
                   35                                  40                                  45

Phe Val Arg Phe Arg Lys Ala Gly Phe Ser Trp Pro Leu Pro Ala Gly  
       50                                  55                                  60

Met Ser Glu Arg Glu Leu Asp Gly Arg Leu Tyr Gly Ser Thr Ser Thr  
       65                                  70                                  75                                  80

Val Pro Val Val Leu Cys Ser Gly Ser Val Ile Gln Asp Thr Ser Lys  
                   85                                  90                                  95

Ser Cys

<210> 48  
 <211> 106  
 <212> PRT  
 <213> Escherichia coli

<400> 48  
 Met Ile Lys Thr Arg Arg Thr Lys Arg Thr Phe Ser Pro Glu Phe Lys  
       1                                  5                                  10                                  15

Leu Glu Ala Phe Glu Gln Val Val Val Lys Tyr Gln Arg Asp Val Arg  
                   20                                  25                                  30

Glu Val Ala Gln Ala Leu Glu Leu Asn Pro Asp His Leu Arg Lys Trp  
           35                          40                          45  
 Ile Arg Leu Tyr Lys Gln Glu Leu Gln Gly Ile Glu Pro Ala Gly Asn  
           50                          55                          60  
 Ala Ile Thr Pro Glu Gln Arg Glu Ile Gln Gln Leu Lys Ala Gln Ile  
           65                          70                          75                          80  
 Lys Arg Val Glu Met Glu Lys Glu Ile Leu Lys Gln Ala Ala Val Leu  
                           85                          90                          95  
 Met Ser Glu Ile Pro Gly Lys Leu Ser Arg  
                           100                          105

<210> 49  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Oligonucleotide

<400> 49  
 tgctctagag ccattactca gaatggg 27

<210> 50  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Oligonucleotide

<400> 50  
 cgcgagctcg acgactgaat gatccc 26

<210> 51  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:Oligonucleotide

<400> 51  
 tccccgggt actgcagcac tcaacc 26

<210> 52  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligonucleotide

<400> 52  
gatcccgga ccactgaaat gcgtgc 26

<210> 53  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligonucleotide

<400> 53  
tcgtctagag atgatggtga tggagcg 27

<210> 54  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligonucleotide

<400> 54  
gaactgcagc caaatactga taccaccc 28

<210> 55  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligonucleotide

<400> 55  
gaactgcagg ctaaaacaga agacgcg 27

<210> 56  
<211> 27

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligonucleotide

<400> 56  
catgcatgca ctccatatga caaccgc 27

<210> 57  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligonucleotide

<400> 57  
tcgtctagaa tgaagctgcg catgagg 27

<210> 58  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligonucleotide

<400> 58  
caactgcagt cgcaaattgc gaactgg 27

<210> 59  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligonucleotide

<400> 59  
caactgcaga ccgcaacttt tcgacgc 27

<210> 60  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligonucleotide

<400> 60  
catgcatgcc agtgagccat tgttccc 27

<210> 61  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligonucleotide

<400> 61  
tgctctagat acgactctga caggagg 27

<210> 62  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligonucleotide

<400> 62  
tcagatatca actaccagca gtttgg 26

<210> 63  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligonucleotide

<400> 63  
tcagatatcc ataaagagtg acgtggc 27

<210> 64  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligonucleotide

<400> 64  
tgctctagaa aacgtggcaa cagagcg 27

<210> 65  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligonucleotide

<400> 65  
tgctctagaa ggcgttgctg atcctg 26

<210> 66  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligonucleotide

<400> 66  
gaactgcagg aaaaggccga gcagactg 28

<210> 67  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligonucleotide

<400> 67  
gaactgcagt acagccatgt ttacggt 27

<210> 68  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligonucleotide

<400> 68  
catgcatgcg gtgtacgaca gtttgcg 27

<210> 69  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligonucleotide

<400> 69  
tgctctagac acatcatggg cacacc 26

<210> 70  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligonucleotide

<400> 70  
gaactgcaga accgtccaca tcaggcg 27

<210> 71  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligonucleotide

<400> 71  
gaactgcaga ccctgcttgc cattccg 27

<210> 72  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:Oligonucleotide

<400> 72  
catgcatgca taagcgtcga acaggcg 27